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.A_Geneseq_16Dec04:*
1: geneseqp1990s:*
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3: geneseqp2000s:*
4: geneseqp2001s:*
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2290
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Listing first 45 summaries
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and is derived by a Pred. No. is the number of results predicted by chance to have a ster than or equal to the score of the result being printed, rived by analysis of the total score distribution.

SUMMARIES

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2 8	Score	Query Match	Length	DB	ID	Description
1	2290	100.0	421	ا م	AAE00826	Aae00826 Murine ha
N	2279.5	9	422	N	AAY05782	2 Human t
w	27	99.5	422	N	AAY06479	9 Human
4.	2279.5	99.5	422	N	AAY17825	5 Human
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o	2279.5	99.5	422	w	AAB01316	6 Human
7	2279.5	99.5	422	w	AAY93686	Amino
œ	2279.5	99.5	422	4.	AAG63545	5 Amino
9	279	99.5	422	σ	ABU55925	Human
10	2279.5	99.5	422	σ	ABU60235	Human
11	2279.5	99.5	422	თ	ABG72776	Abg72776 Human cyt
12	2279.5	99.5	422	0	ABU64921	Human
13	2279.5	99.5	422	σ	ABU58355	Novel
14	2279.5	99.5	422	σ	ABU57241	Abu57241 Human PRO
15	2279.5	99.5	422	σ	ABU56306	Abu56306 Human sec
16	2279.5	99.5	422	6	ABU60346	Abu60346 Novel hum
17	2279.5	99.5	422	σ	ABU11307	-
18	2279.5	99.5	422	o	ABU67126	
19	2279.5	99.5	422	7	ADC25788	
20	2279.5	99.5	422	7	ADC25546	Adc25546 Human sec
21	2279.5	99.5	422	7	ADC25667	Adc25667 Human sec
22	2279.5	99.5	422	7	ADH27452	Adh27452 Human sec
23	2279.5	99.5	422	œ	ADE71501	1 Human
24	2279.5	99.5	422	œ	ADG63444	Human
25	2279.5	99.5	422	œ	ADH43173	Human

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Aae00821	Aay93659	Aaw55012	Aag63544	Aay28281	Abb06125	Adt61032	Adt 90844	Adc07179	Aab36647	Aab19588	Aay29779	Aaw70861	Adr41505	Aay26338	Aaw59805	Aaw70860	Adq18851	Adn00411	2020
Murine ha	A murine	Novel hae	Amino aci	Amino aci	Human NS	Human cyt	Human DNA	Allelic v	Human CD-	Human U4	Amino aci	Human Zcy	Human sof	Human sec	TANCOLT				

ALIGNMENTS

Murine haemopoietin receptor, NR6 protein, encoded by NR6 DNA. 09-SEP-2004 02-JUL-2001 AAE00826; AAE00826 standard; protein; 421 AA. (revised) (first en entry)

Murine; biologically active complex; haemopoietin receptor; NR6; cardiotrophin-like cytokine; CLC; therapy; prophylaxis; proliferation; differentiation; cell survival; neurotrophic activity.

мив вр. Unidentified.

WO200127157-A1

19-APR-2001.

06-OCT-2000; 2000WO-AU001216

08-OCT-1999; 99AU-00003327. 12-MAY-2000; 2000AU-00007489.

(AMRA-) AMRAD OPERATIONS PTY LTD

Nakata Y, Nash A, Jachno KM, Hasegawa 3 Fabri LJ, Reid ζ, Bartlett PF, Hilton DJ;

WPI; 2001-281978/29. N-PSDB; AAD04199.

New biologically active complex comprising NR6 and cardiotrophin-like-cytokine, for facilitating proliferation, differentiation and/or survival of a cell.

Claim 29; Page 106-107; 123pp; English.

The present invention relates to a biologically active complex comprising a haemopoletin receptor, NR6 and cardiotrophin-like cytokine (CLC). The complex is useful in the manufacture of a medicament for the treatment and/or prophylaxis of a subject, as it is involved in facilitating proliferation, differentiation and/or survival of a cell. The complex or its components have neurotrophic activity. The present sequence is murine haemopoletin receptor, NR6 protein, encoded by NR6 DNA

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RESULT 2
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  16-OCT-1997;
                        14-OCT-1998;
                                                                                                                                                                              Homo
                                                                                                                                                                                                      antiinflammatory;
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  97GB-00021961.
                          98WO-EP006497
                                                                                              38. .422 /note= "mature protein; a polypeptide comprising acids 38-422 is also claimed in Claim la"
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RESULT 3
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Matches 421
                                                                                                                                                                                                                                                                             This sequence represents human PRO327 (UNQ288), a 46.3 kDa protein (pI 9.42) encoded by the novel cDNA clone DNA38113 (see AAX87256).

Amplification of DNA38113 occurs in various lung and colon tumours and cell lines, suggesting a significant role in tumour formation and growt Antagonists (e.g. antibodies) directed against PRO327 are expected to have utility in cancer therapy. The invention identifies 14 genes (see AAX87254-67) that are amplified in the genome of tumour cells. Such amplification is expected to be associated with overexpression of the gene product and to contribute to tumorigenesis. The encoded proteins (see AAX06477-90) may be useful targets for the diagnosis and/or treatment (including prevention) of certain cancers, and may act as predictors of the prognosis of tumour treatment. Antibodies that bind t proteins are claimed and used in claimed cancer diagnostic kits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-APR-1998
22-MAY-1998
10-JUN-1998
10-NOV-1998
20-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antibody against proteins diagnosis and treatment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human tumour-associated protein
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                                                                                                                                                                     MPAGRRGPAAQSARRPPPLLP-LLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC
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             DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD
                                                                GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ
                                                                                                                  SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD
                                                                                                   SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD
                                                                                                                                                     MPAGRRGPAAQSARRPPPLLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC
                                                                                                                                                                                                                                                           422 AA;
DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD
                                                 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fig 6; 162pp; English
                                                                                                                                                                                                         Conservative
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98US-0083500P.

98US-0086414P.

98US-0088742P.

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                                                                                                                                                                                                                    Score 2279.5;
Pred. No. 3.4
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RESULT 4
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17-DEC-1997;
18-DEC-1997;
transmembrane proteins used therapeutically. The PRO proteins have cytostatic, anti-inflammatory, anti-proliferative and immunosuppressive activity. The proteins and polynucleotides can be used in therapy, identification of homologues, raising antibodies and design of probes and primers. They can be used in a range of diseases related to proteins that they have homology with, e.g. a PRO protein having homology to complement proteins may be used in inflammatory responses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY17825 standard; protein; 422 AA.
                                                                                                                                                                       The present invention describes nucleic acids
                                                                                                                                                                                                                     Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRO protein; tumour necrosis factor family; TNF; cytokin ed protein; transmembrane protein; inflammation disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                              GENENTECH
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Human U4 protein; haematopoietin receptor superfamily; biological activity; cytokine; cell proliferation; cell differentiation; immune stimulation; immune suppression; haematopoiesis regulation; immune disorder; immune deficiency; autoimmune disorder; allergy; cancer; myeloid cell; lymphoid cell deficiency; platelet disorder.
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                                                   WPI; 1999-611303/52.
                                                                                                  Donaldson D,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILPSGRRGTARGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWWQKSHKTRNQDEGILPSGRRGTARGP
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Pred. No. 3.4e-184;
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Human 25-SEP-2000 AAB01316;

PRO327

polypeptide (first

entry)

AAB01316 standard;

protein;

422

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PRO; membrane bound protein; secreted protein; PRO357; PRO327; PRO243; PRO715; PRO241; PRO323; PRO299; PRO233; PRO344; PRO347; PRO355; PRO353 PRO361; PRO365; transmembrane polypeptide; antibody; screening; detection; inhibition; probe; primer; human.

Key Peptide

Location/Qualifiers

Signal peptide

Homo sapiens

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel polypeptides and polynucleotides used for treatment of human diseases and disorders e.g. immune disorders or deficiencies caused fungal, parasitic or viral infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILPSGRRGTARGP
                                                                                                                                                                           VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG
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                                                    GPVRRELKQF1GWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEG1LPSGRRGTARGP
                                                                                                        LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS
                                                                                                                          LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS
                                                                                                                                                              VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG
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Pred. No. 3.4
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01-DEC-1998;
16-DEC-1998;
22-DEC-1998;
                                                                   Baker KP, Botstein D,
Gerritsen ME, Goddard
Hillan KJ, Kljavin IJ,
      Claim 12;
                          New human nucleic
designated as PRO
                                               N-PSDB;
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98US-0112850P.
98US-0113296P.
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                                                                   Eaton DL, Ferrara N, Filvaroff E;
1, Godowski PJ, Grimaldi CJ, Gurn
Napier MA, Roy MA, Tumas D, Woo
     English
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PRO1017;
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                                                                                     Modified-site
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                                                                                                                                                                                                                                                                                                Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amino acid sequence of novel polypeptide PRO327
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                                                                                                                                                                                                                                                                                                                                              PRO292; PRO327; PRO1265; PRO344; PRO343; PRO347; PRO357; PRO715; PRO1112; PRO509; PRO853; PRO882; tumour cell; tumourigenesis; neoplastic cell growth; cell proliferation.
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08-MAR-1999;
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121. .127
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413. .417
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   RESULT 8
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ID AAG63545
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XW NNT-
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Matches 421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New anti-polypeptide antibody useful in the treatment neoplastic cell growth and proliferation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mammals
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421
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                                                                                    GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ
                                                                                                                                                                                                                                                                                                                                                                                              SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALANLNGSRQRSGDNLVCHARD
                                                                                                                                                                                                                                                                                                                                                                                                                      SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALLANLNGSRQRSGDNLVCHARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MPAGRRGPAAQSARRPPPLLPLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MPAGRRGPAAQSARRÞÞÞILLP-LLLLCVLGAPRAGSGAHTAVISPQÞFILLIGSSLLATC
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                             AR 421
                                                               GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILPSGRRGTARGP
                                                                                                                                                                                              VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG
                                                                                                                                                                                                                                                                                  DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD
                                                                                                                                                                                                                                                                                                                               GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ
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                                                                                                                              LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS
                                                                                                                                                   LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS
                                                                                                                                                                                                                   VHVSRVGGLEDQLSVRWVSPPALKDFLPQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG
                                                                                                                                                                                                                                                               DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD
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Pred. No. 3.4e-184;
D; Mismatches 0;
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XX NNT-1; CLF-1; sCNTFRalpha; nervous system; neuron; nervous system; KW NNT-1; CLF-1; sCNTFRalpha; nervous system; neuron-muscular function; tumour; immune system; haematopoietic system; KW reproductive system; liver; skeletal muscle; neurodegenerative disease; KW amyotrophic lateral sclerosis; Parkinson's disease; Huntingdon's disease; KW muscular mass; paralysis; cancer; obesity; fertility; endometriosis; KW blastocyst implantation; thrombosis; retinal disease; KW retinal pigmentosis.

protein.

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CC describes a complex comprising a NNT-1 protein and a CLF-1 and/or CC scNTFRalpha, protein. The NNT-1/CLF-1 complex is used to modulate activity of the sCNTFRalpha/gp130/LIFRbeta receptor complex, or to induce CC phosphorylation of the tyrosine of gp130 and LIFRbeta, particularly where CC cells expressing the receptor complex are in the central or peripheral carrous system, in neurons implicated in neuro-muscular function or in CC skeletal muscle. The complex or antibodies are also used to decrease the survival, growth or proliferation of tumour cells or to facilitate the proliferation and/or inhibit differentiation of cells stocks. The complex CC is also used to modulate activity of the gp130/LIFRbeta receptor or cells cexpressing that receptor, particularly those cells implicated in the CC immune, haematopoietic, nervous or reproductive system, the liver or CC skeletal muscle. Molecules of the invention may be used to prevent or treat neurodegenerative diseases including amyotrophic lateral sclerosis, CC parkinson's and Huntington's disease, to repair or regenerate nervous or may also be used to treat cancer, obesity and associated diseases, and to complex implantation, thrombosis, or retinal disease, particular CC retinal picmentosis, thrombosis, or retinal disease, particular
                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A complex comprising a NNT-1 protein and a CLF-1 and/or sCNTFRalpha protein useful to treat neurodegenerative disease including Parkins and Huntington's, obesity and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     retinal pigmentosis
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12-OCT-2000;
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INSERM INST NAT SANTE & RECH MEDICALE.
                                                                                                                                                                                                                                                                                                      MPAGRRGPAAQSARRPPPLLP-LLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC
               VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG
                                                                                    DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD
                                                                                                                                                              GSILAGSCLYVGLÞÞEKÞVNISCWSKNMKDLTCRWTÞGAHGETFLHTNYSLKYKLRWYGQ
                                                                                                                                                                                                               SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD
                                                                                                                                                                                                                                    SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD
                                                                                                                                                                                                                                                                                                                                                                                                                                      422 AA;
VHVSRVGGLEDQLSVRWVSPPALKD
                                                                                                                                                                                                                                                                                     MPAGRRGPAAQSARRPPPLLPLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC
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                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence represents a human CLF-1 protein. The specification
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2000FR-00013089
                                                                                                                                                                                                                                                                                                                                                                            99.5%;
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                                                                                                                                                                                                                                                                                                                                                           Score 2279.5; DB 4
Pred. No. 3.4e-184;
0; Mismatches 0;
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The invention relates to an isolated PRO polypeptide (a secreted transmembrane protein) comprising: (a) at least 80% sequence ider positives when compared to any of 15 sequences, fully defined in

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Fig 14;

178pp;

English

and diabetes.

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22-FEB-2000;
02-MAR-2000;
30-MAR-2000;
22-MAY-2000;
28-JUL-2000;
                                                                                                                                                                                                                                                                                                              16-SEP-1998;
01-DEC-1998;
01-DEC-1998;
22-JUN-1999;
15-SEP-1999;
30-NOV-1999;
                                                         New isolated PRO polypeptide and encoding nucleic acid, useful for the diagnosis and treatment of disorders associated with the PRO polypeptisuch as AIDS, cancer, atherosclerosis, inflammatory disease and diabet
                                                                                                                                 Baker KP, Botstein D,
Gerritsen ME, Goddard
Hillan KJ, Kljavin IJ,
                                                                                                     WPI; 2003-174141/17.
N-PSDB; ABX75462.
                                                                                                                                                                                                                                                                                          01-DEC-1999;
16-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytostatic; antiarteriosclerotic; antiinflammatory; antidiabe cardiant; AIDS; acquired immunodeficiency syndrome; cancer; atherosclerosis; inflammatory disease; diabetic complication;
                                                                                                                                                                                                                                                                                                                                                                                       31-AUG-2001; 2001US-00944654
                                                                                                                                                                                                                                                                                                                                                                                                            03-OCT-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard;
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                                                                                                                                                                                            99WO-US028301.
99WO-US038095.
2000WO-US003565.
2000WO-US004414.
2000WO-US00843.
2000WO-US00843.
2000WO-US014042.
2000WO-US0166667.
2000WO-US02678.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    secreted protein; transmembrane protein; anti-HIV;
antiarteriosclerotic; antiinflammatory; antidiabet
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99WO-US021090.
99WO-US028313.
99WO-US028409.
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A, Godowski
Napier MA,
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                                                                                                                                  PJ,
Roy
                                                                                                                                 ra N, Filvaroff E;
Grimaldi JC, Gurn
MA, Tumas D, Woo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antidiabetic;
                                                                                                                                  Gurney AL; Wood WI;
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RESULT 10
ABU60235
ID ABU60
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AC ABU60
XT
AC ABU60
DT 24-AF
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Human
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KW Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 421
                                            Human PRO polypeptide
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Human; PRO; secreted polypeptide; transmembrane polypeptide; cancer;
                                                                                             24-APR-2003
                                                                                                                                                                                        ABU60235
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묽 Ş 밁 Ś 밁 8 밁 δ 밁 S 밁 S 밁 Ś 밁 Ś

Gerritsen | Hillan KJ,

n ME, oc AT. Kljavin)

Botstein D, Ea ME, Goddard A, Kljavin IJ, N

Eaton DL, Ferran 1, Godowski PJ, Napier MA, Roy

Ferrara N, Filvaroff E; i PJ, Grimaldi JC, Gurn, Roy MA, Tumas D, Woo

Gurney Wood W Y AL; ~

GENENTECH

WPI; 2003-174088/17. N-PSDB; ABX89453.

The invention relates to a human secreted and transmembrane polypeptide (PRO) and the polynucleotide encoding it. The PRO polypeptide or polynucleotide is useful in pharmaceuticals, diagnostics, biosensors or bioreactors. These are particularly useful for detecting or treating

Claim

Fig

14;

173pp;

English.

New secreted and transmembrane polypeptides (e.g. PRO241, for use in pharmaceuticals, diagnostics or bioreactors, particularly for detecting or treating e.g. cancers, infertility or acquired immunodeficiency syndrome in mammals.

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16-DEC-1997
16-DEC-1997
16-DEC-1997
17-DEC-1997
17-DEC-1997
18-DEC-1997
18-DEC-1998
09-FEB-1998
16-DEC-1998
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16-DEC-1998
16-DEC-1998
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22-JUN-1999
23-JUN-1999
23-JUN-1999
15-SEP-1999
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11-DEC-1997;
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990S-0146229P
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990C-US012313
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990C-US028313
990C-US028313
990C-US028313
990C-US0304941
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Best Local
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                                                                                                       Human; gene expression; bone formation; cartilage formation; embryonic development; cytokine receptor-like factor 1; CLFF-1; CLRF-1; mesenchymal cell differentiation; matrix metalloproteinase 23; MMP23; bone development; antagonist; agonist; cadherin; CD68; cytokine; bone development; antagonist; agonist; cadherin; CD68; cytokine; diagnosis; osteodystrophy; osteohypertrophy; osteoblastoma; osteoperia; osteolytic lesion; hypercalcaemia of malignancy; Paget's disease; hyperparathyroidism; hypercalcaemia of malignancy; limmobilisation; sex hormone deficiency; inflammatory disease; rheumatoid arthritis; osteoarthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancers, inflammatory diseases, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, acquired immunodeficiency syndrome (AIDS) and diabetic complications in mammals, e.g. humans, dogs, cats, cattle, horses, sheep, pigs, goats or rabbits. The sequences are also useful in biotechnological and medical research and in various industrial applications. Sequences ABU60230-ABU60245 represent human PRO polypeptides of the invention
                   WO200285285-A2
                                                                                                                                                                                                                                                                                                                                                        20-FEB-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG72776 standard; protein; 422
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AR 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MPAGRRGPAAQSARRPPPLLP-LLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAMMQKSHKTRNQDEGILPSGRRGTARGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MPAGRRGPAAQSARRPPPLLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILPSGRRGTARGP 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LKPGTVYFVQVRCNPFG1YGSKKAG1WSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VHVSRVGGLEDQ!
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                                                                                                                                                                                                                                                                                                                       receptor-like factor 1 (CLF-1 or CLRF-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.5%;
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Pred. No. 3.4e-184;
D; Mismatches 0;
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CC essential process in embryonic development and plays a critical role in CC many diseases and conditions in humans. Two genes found to be regulated CC during bone and cartilage formation are the cytokine receptor-like factor CC (CLF-1 or CLRF-1), which is specifically regulated during mesenchymal CC ell differentiation, and matrix metalloproteinase 23 (MMP23), which is generations comprising a number of expression of a number of genes, CC computer program for ranalysing levels of expression of a number of genes, CC compositions comprising a number of antagonists or agonists of the genes CC and methods for determining whether a subject has, or is likely to CC develop, a disease related to bone or cartilage resorption or formation, CC for determining the effectiveness of a treatment intended to stimulate CC bone or cartilage formation or resorption, for identifying a compound for CC cartilage formation possibly acting a disease related to bone or cartilage formation possibly acting as a cadherin or CD68 agonist or a CC cytokine antagonist. The methods and compositions are useful for CC diagnosing and treating disorders associated with bone or cartilage (costeoplas osteopertrusis, osteogenesis imperfecta, osteoporosis, osteoplas osteopartrusis, osteogenesis imperfecta, osteoporosis, CC osteoplas osteopartrusis, osteogenesis imperfecta, osteoporosis, CC immobilisation or sex hormone deficiency, bone and cartilage loss caused CC by an inflammatory disease, rheumatoid arthritis, osteoarthritis and bone CC fractures. The sequence presented is the human CLF-1 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Determining the difference between levels genes, useful for diagnosing and treating or cartilage formation or resorption such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention discloses a method for determining the difference between the levels of expression of a number of, at least 500 genes, during bon or cartilage formation. The method comprises determining levels of RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-APR-2002; 2002WO-US012149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from the genes to obtain levels of expression and comparing these to a set of reference levels for each of the genes. Bone formation is an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 192-193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              197pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of expression of a number disorders associated with as osteoporosis and bone
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of bone

밁 8 밁 Ś 밁 S 밁 S Query Match Best Local S Matches 421 181 121 421; 180 120 61 6 Similarity GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ MPAGRRGPAAQSARRPPPLLP-LLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD MPAGRRGPAAQSARRPPPLLPLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALANLNGSRQRSGDNLVCHARD Conservative 99.5**%**; 0 Score 2279.5; Pred. No. 3.4 Mismatches .4e-184; DB 6; Indels Length 422; ۲, Gaps 179 119 240 239 120 60

240

VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG

Sequence

422

AA;

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RESULT 12
ABU64921
ID ABU64921
ID ABU64921
AC ABU64
AC ABU64
AC ABU64
AC Human
XX Human
XX Human
XX Human
XX Homo
OS Homo
VX 21-NC
XX 21-NC
YX 31-AU
PPR 11-DE
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  18-DEC-1997
05-JAN-1998
09-FEB-1998
25-FEB-1998
16-SEP-1998
11-DEC-1998
01-DEC-1998
02-JUN-1999
12-JUN-1999
15-SEP-1999
15-SEP-1999
15-SEP-1999
16-DEC-1999
16-DEC-1999
11-FEB-2000
02-MAR-2000
03-MAR-2000
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12-DEC-1997;
16-DEC-1997;
16-DEC-1997;
16-DEC-1997;
16-DEC-1997;
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11-DEC-1997;
11-DEC-1997;
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Cornelia de Lange syndrome; gene therapy; immune disorder;
inflammatory disease; organ failure; atherosclerosis; cardiac injury;
infertility; birth defect; premature aging; cardiac injury; AIDS; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABU64921;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human secreted/transmembrane protein PRO327.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-MAY-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard; protein; 422
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2000WO-US003565.
2000WO-US004414.
2000WO-US005841.
2000WO-US005849.
2000WO-US014042.
2000WO-US0120710.
2000WO-US032678.
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98US-0113296P
99WO-US012252
99US-0146222P
99WO-US021090
99WO-US028313
99WO-US028409
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97US-0069425P
97US-0069694P
97US-0069696P
97US-0069702P
97US-0069870P
97US-0069873P
97US-0069873P
97US-0069873P
97US-0070440P
98US-00774486P
98US-00774086P
98US-00774092P
98US-0075935
98WO-US015330
98WO-US015330
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97US-0069334P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 12; Fig 14; 172pp; English.
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25-MAY-2001; 2001US-00866028
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      360 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILPSGRRGTARGP
                                            301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MPAGRRGPAAQSARRPPPLLF-LLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            n ME, Goun.
W, Kljavin IJ,
                                          LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS
                                                                LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS
                                                                                                                       VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG
                                                                                                                                         VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG
                                                                                                                                                                                                  DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD
                                                                                                                                                                                                                          DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD
                                                                                                                                                                                                                                                                               GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ
                                                                                                                                                                                                                                                                                                          GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ
                                                                                                                                                                                                                                                                                                                                                            SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALANLNGSRQRSGDNLVCHARD
                                                                                                                                                                                                                                                                                                                                                                                               SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALANLNGSRQRSGDNLVCHARD
                                                                                                                                                                                                                                                                                                                                                                                                                                   MPAGRRGPAAQSARRPPPLLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC
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Pred. No. 3.4e-184;
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0, 6

Indels Length

Gaps

299 240

359 300 180

119

60

120

422; 1;

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The invention relates to an isolated nucleic acid encoding a secreted/
CC transmembrane polypeptide (designated as PRO proteins). 15 PRO
CC polypeptides and their encoding polynucleotides are disclosed. Also
CC included are a vector comprising the PRO nucleic acid, a host cell
CC comprising the vector, a process for producing a PRO polypeptide (by
CC culturing the host cell under conditions for the expression of the PRO
CC polypeptide, and recovering the PRO polypeptide from the cell culture, an
CC isolated polypeptide having at least 80% amino acid sequence identity to
CC the PRO polypeptides, a chimaeric molecule comprising PRO fused to a
CC the PRO polypeptides, a chimaeric molecule comprising PRO fused to a
CC the PRO polypeptides, a chimaeric molecule comprising PRO fused to a
CC the PRO polypeptides, a chimaeric molecule comprising PRO fused to a
CC the PRO polypeptide sequence are useful as hybridisation probes,
CC in chromosome and gene mapping, in generating sense and antisense RNA or
CC DNA, in generating transgenic or knock-out animals which can be used in
CC the development and screening of therapeutically useful reagents, and in
CC gene therapy. The polypeptides may be used as molecular weight markers
CC for protein electrophoresis purposes. The PRO polypeptides and nucleic
CC acids may also be used for chromosome identification, and tissue typing.
CC gene therapy proteins are variously implicated in immune
CC disorders, inflammatory disease, organ failure, atherosclerosis, cardiac
CC injury, infertility, birth defects, premature aging, cardiac injury,
CC ALDS, cancer and diabetic complications. The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New transmembrane polypeptides and polynucleotides useful for chromosome identification, tissue typing, gene therapy, in chromosome and gene mapping, or as molecular weight markers.
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A, Godowski PJ, Grima...
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Grimaldi JC, Gurn
MA, Tumas D, Woo
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RESULT 13
ARUS8355
ID ARUS88
ID ARUS88
XX ARUS8
AC ARUS8
AC ARUS8
XX DT 14-AR
XX Human
XX Human
XX Homo
XX O'C'O'
XX O'C'O'C'
XX O'C'C'
XX O'C'O'C'
XX O'C'
XX O'C'O'C'
XX O'C'
XX O'C'O'C'
XX O'C'O'C'
XX O'C'
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XX
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18-DEC-1997;
05-JAN-1998;
09-FEB-1998;
09-FEB-1998;
16-SEP-1998;
16-DEC-1998;
16-DEC-1998;
16-DEC-1998;
22-DEC-1998;
22-DEC-1998;
23-MAR-1999;
23-JUL-1999;
15-SEP-1999;
15-SEP-1999;
16-DEC-1999;
11-FEB-2000;
22-FEB-2000;
22-MAR-2000;
22-MAY-2000;
28-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; antiinflammatory; antiarteriosclerotic; cardiant; gynecologica anti-HIV; cytostatic; antidiabetic; BMP-agonist; BMP-Antagonist; cytostatic; antidiabetic; BMP-agonist; pen-Antagonist; cytostine-antagonist; gene-Therapy; inflammatory disease; organ failure; atherosclerosis; cardiac injury; infertility; birth defect; premature aging; AIDS; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-DEC-1997;
11-DEC-1997;
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   GENENTECH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complication.
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                                  97US-0069425P

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97US-0069873P

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97US-0069817P

98US-0074086P

98US-0074086P

98US-0074092P

98US-00112850P

98US-0112850P

98US-0112850P

98US-0112851P

98US-0112851P

98US-0112851P

99US-0254311

99US-0146222P

99WO-US01293

99WO-US02193

99WO-US02193

12000WO-US028311

2000WO-US028311

2000WO-US028311
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RESULT 14
ABU57241
ID ABU57
XX
AC ABU57
XX
AC ABU57
XX
DT 04-AF
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DT 04-AF
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Humar
XX
Humar
KW Anti-
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Hillan KJ,
Human; antiinflammatory; antiarteriosclerotic; cardiant;
anti-infertility; anti-HIV; cytostatic; antidiabetic; tr
                                                     Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 422
                                                                                                                            ABU57241;
                                                                                                                                                             ABU57241 standard; protein;
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                                                                                                                                                                                                                                                         421
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                                                      PRO327
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                                                                                                                                                                                                                                                                                          421
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Query Match
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Matches 421; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated PRO polypeptide and encoding nucleic acids, useful for the diagnosis and treatment of disorders such as inflammatory disease, atherosclerosis, cardiac injury, infertility, AIDS, cancer and diabetic
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DB; ABX78444.
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П. Kljavin э
                             GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILPSGRRGTARGP
                                                                                                                                LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS
                                                                                                                                                                                                                                  VHVSRVGGI.EDQLSVRWVSPPALKDFLFQAXYQIRYRVEDSVDWKVVDDVSNQTSCRLAG
                                                                                                                                                                                                                                                                                                                                        DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MPAGRRGPAAQSARRPPPLLP-LLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC
GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILPSGRRGTARGP
                                                                                                  LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS
                                                                                                                                                                                                     VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG
                                                                                                                                                                                                                                                                                                             DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD
                                                                                                                                                                                                                                                                                                                                                                                                                GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MPAGRRGPAAQSARRPPPLLPLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC
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Æ, Goddard
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A, Godowski
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 2279.5; DB 6;
Pred. No. 3.4e-184;
0; Mismatches 0;
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i PJ, Grimaldi JC, Gurney AL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
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422 AA

transmembrane;

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Best Local S
Matches 421
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01-DEC-1999;
22-JUN-1999;
15-SEP-1999;
30-NOV-1999;
30-NOV-1999;
01-DEC-1999;
11-FEB-2000;
22-FEB-2000;
22-FEB-2000;
22-MAR-2000;
22-MAR-2000;
22-MAY-2000;
28-JUL-2000;
28-FEB-2001;
28-FEB-2001;
28-FEB-2001;
28-FEB-2001;
28-FEB-2001;
28-FEB-2001;
28-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       premature
                                                                                                                                                                                         This invention relates to a nucleotide sequence encoding an isolated secreted and/or transmembrane protein. The nucleotide sequences of the invention may have antiinflammatory, antiarteriosclerotic, cardiant, anti-infertility, anti-HIV, cytostatic and antidiabetic activities and may be used in gene therapy. The nucleic acids and polypeptides are useful for treating inflammatory diseases, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, cancer, or diabetic complications. The nucleic acids are useful as hybridisation probes, in chromosome and gene mapping, and in generating antisense RNA or DNA. The polypeptides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. Both are useful in tissue typing. The present sequence represents a protein encoded by the nucleic acids of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US2002142958-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antiinflammatory; anti-HIV; antiarteriosclerotic; cardiant; infertility; anti-infertility; cytostatic; antidiabetic; gene therapy; birth defect; inflammatory disease; organ failure; atherosclerosis; cardiac injury; premature aging; AIDS; cancer; diabetic complication.
                                                                                                                                                                                                                                                                                                                                                                                                                        as PRO,
cardiac
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Hillan KJ, Kljavin
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                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                    secreted
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DB; ABX77077.
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                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                 421;
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                                                                                                                                                                                                                                                                                                                                                                                                                     reted and transmembrane nucleic acids and polypeptides, designated useful for treating inflammation, organ failure, atherosclerosis, injury, infertility, birth defects, premature aging, AIDS, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENENTECH INC.
                                                                                                              Similarity
                                                                                                                                                       422
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                                       MPAGRRGPAAQSARRPPPLLP-LLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC
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SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD
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99WO-US01255108.
99WO-US012552.
99WO-US021090.
99WO-US028313.
99WO-US028301.
99WO-US03565.
2000WO-US003565.
2000WO-US0035641.
2000WO-US00841.
2000WO-US008439.
2000WO-US008439.
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                                                                                                              99.5%;
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A, Godowski PJ, Grimaldi JC, Gurn
Napier MA, Roy MA, Tumas D, Woo
                                                                                                 Score 2279.5;
Pred. No. 3.4e
0; Mismatches
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                                                                                              5; DB 6;
3.4e-184;
0;
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                                                                                                                           Length
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Wood WI;
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RESULT 15
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AC ABU56
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12-DEC-1997;
16-DEC-1997;
16-DEC-1997;
16-DEC-1997;
17-DEC-1997;
17-DEC-1997;
18-DEC-1997
05-JAN-1998
09-FEB-1998
09-FEB-1998
25-FEB-1998
16-SEP-1998
01-DEC-1998
01-DEC-1998
22-DEC-1998
02-DEC-1999
02-JUN-1999
28-JUL-1999
15-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gynecological; anti-HIV; cytostatic; antidiabetic; inflammatory disease; organ failure; atherosclerosis; cardiac injury; infertility; birth defect; premature aging; AIDS; acquired immunodeficiency syndrome; cancer; diabetic complication.
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11-DEC-1997
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al; anti-HIV; cytostatic; antidiabetic; inflammatory
re; atherosclerosis; cardiac injury; infertility;
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    970S-0069334P.
970S-0069335P.
970S-0069694P.
970S-0069696P.
970S-0069870P.
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980S-0074098P.
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980S-0113296P.
990S-0146222P.
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97US-0069278P
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N-PSDB; ABX75909.
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                                                                                                                                                                    SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARD
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                                                                                                                                                                                                                                                            MPAGRRGPAAQSARRPPPLLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC
                    DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD
                                                                                                                                                                                                                                                                                                                                                                                                                                         422 AA;
DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD
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A, Godowski PJ, Grimaldi JC, Gurn
Napier MA, Roy MA, Tumas D, Woo
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                                                                                                    LKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS
                                                                                                                 LKPGTVYFVQVRCNPFG1YGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSS
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Result No.

Database

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recept	S74225	N	895	8.0	184	5
MPL-P protein prec	A45266	N	635	8.1	186.5	4.
MPL-K protein prec	B45266	N	579	8.1	186.5	ü
differentiation-st	JX0312	N	1092	8.2	187	2
proto-oncogene - m	S37622	N	626	8.3	190	Ξ
leptin receptor, O	PC4184	N	1162	8.3	190.5	ö
lactogen receptor	B34631	N	150	8.3	191	9
'interleukin-6 rece	JL0144	N	440	8.4	191.5	8
hematopoietic grow	S35317	N	625	8.5	194	7
leptin receptor, s	S68438	N	1162	8.5	194.5	9
leptin receptor, s	S68440	N	900	8.5	194.5	ភ
leptin receptor, s	S68437	N	894	8.5	194.5	4
leptin receptor, s	868439	N	892	8.5	194.5	ũ
leptin receptor, s	S68441	N	805	8.5	194.5	ະ
prolactin receptor	A32868	N	156	8.7	199	ř
interleukin-6 rece	JL0145	ν	460	8.7	199.5	õ

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CY 295 CRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTP 338	Db 133 LAV-EVKQPEDRKPYLWIKWSPPTLIDLKTGWFTLLYEIRLKPEKAAEWE-IHFAGQQTE 190	QY 240 VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTS 294	Db 73 HECPDYITGGPNSCHFGKQYTSMWRTYIMMVNATNQMGSSFSDELYVDVTYIVQPDPPLE 132	YHTVGPHSCHIPKD-LALFTPYEIWVEATNRLGSARSDVLTLDILD	Qy 122 ILAGSCLYVG-LPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQD 180 :	Query Match 14.5%; Score 332; DB 2; Length 288; Best Local Similarity 37.1%; Pred. No. 2.1e-18; Matches 83; Conservative 28; Mismatches 95; Indels 18; Gaps 8;	A;Gene: GDB:PRLR A;Gene: GDB:PRLR A;Gene: GDB:PRLR A;Cross-references: GDB:120315; OMIM:176761 A;Map position: 5p13.3-5p13.1 C;Keywords: glycoprotein; transmembrane protein C;Keywords: glycoprotein; transmembrane protein F;12-4/Domain: signal sequence #status predicted <sig> F;25-288/Product: prolactin receptor, short form S1b #status predicted <mat> F;36-221/Domain: cytokine receptor homology <crs> F;59,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted</crs></mat></sig>	A;Status: preliminary A;Molecule type: DNA A;Residues: 1-288 <huz> A;Cross-references: GB:AF214012; PIDN:AF214012.1 C;Comment: This is one of the short forms (Sla and Slb) of the human proactin receptor ta-casein gene promoter activation, with Slb more effective than Sla. However, their li C;Genetics:</huz>	000	A;Molecule type: DNA A;Residues: 1-288 <hu1> A;Residues: 1-288 <hu1> A;Crosa-references: UNIPROT:Q96P36; GB:AF214012; PIDN:AF214012.1 R:Hu. Z.Z.</hu1></hu1>	R;Hu, Z.Z.; Meng, J.; Dufau, M.L. J. Biol. Chem. 276, 41086-41094, 2001 A;Title: Isolation and characterization of two novel forms of the human prolactin recep. A;Reference number: A59405; MUID:21538812; PMID:11518703 A;Accession: B59405 A;Status: preliminary	B59405 B59405 prolactin receptor short form S1b precursor, breast cancer cells T-47D - human C;Species: Homo sapiens (man) C;Species: 1-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004 C:Accession: R59406: R49400	RESULT 1	8.1 635 2 A45266 8.0 895 2 S74225	187 8.2 1092 2 JX0312 differentiation 186.5 8.1 579 2 B45266 MPL-K protein	191 8.3 150 2 B34631 lactogen receptor, 190.5 8.3 1162 2 PC4184 leptin receptor,	194 8.5 625 2 S35317 hematopoietic gro 191.5 8.4 440 2 JL0144 interleukin-6 rec	194.5 8.5 900 2 568448 leptin receptor,	.5 805 2 S68441 leptin .5 892 2 S68439 leptin .5 894 2 S68439 leptin

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prolactin receptor short form S1a precursor, breast cancer cells T-47D - hum (1,5pecies: Homo sapiens (man) (2,5pecies: Homo sapiens (man) (1,5pecies: Homo sapiens (man) (1,5pecies: Homo sapiens (1,5pecies: Lorent sapiens) (1,
A;Title: Identification of a cDNA encoding a long form of prolactin A;Reference number: A40144; MUID:90114212; PMID:2558309 A;Accession: A40144 A;Molecule type: mRNA
                                                                                                                                                                                prolactin receptor long form precursor, hepatoma and breast cance (Species: Homo sapiens (man) C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change C;Accession: A40144; A57018 R;Boutin, J.M.; Edery, M.; Shirota, M.; Jolicoeur, C.; Lesueur,
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A;Residues: 1-376 <HU2>
A;Cross-references: GB:AF214012; PIDN:AF214012.1
A;Cross-references: GB:AF214012; PIDN:AF214012.1
C;Comment: This is one of the short forms (Sla and Slb) of the human prolactin receptor eta-casein gene promoter activation, with Sla less effective than Slb. However, their lited COS-1 and HEK293 cells is due to rapid intracellular turnover of the receptor. #expe
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A;Map position: 5p13.3-5p13.1
C;Keywords: glycoprotein; transmembrane protein
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A;Accession: A49400
A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:Q96P35; GB:AF214012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: A59405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 83
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                                                                                                                                          Boutin, J.M.; Edery, M.; Shirota, M.; bl. Endocrinol. 3, 1455-1461, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :25-376/Product: prolactin receptor, short form S1a #status predicted <MAT>:36-221/Domain: cytokine receptor homology <CRS>:59,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1-24/Domain: signal sequence #status predicted <SIG>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 332; DB z; Pred. No. 2.9e-18;
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                                                                                                                                                                                                                                                                                                                              hepatoma and breast cancer cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -DHGYWSAWSPATFIQIP
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R/Fuh, G.; Wells, J.A.
J. Biol. Chem. 270, 13133-13137, 1995
A;Title: Prolactin receptor antagonists that inhibit the A;Reference number: A57018; MUID:95286597; PMID:7768908
A;Accession: A57018
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                   Cell 63, 1149-1157, 1990
A;Title: Molecular cloning and expression of an IL-6 signal transducer, gp130.
A;Reference number: A36337; MUID:91084844; PMID:2261637
A;Accession: A36337
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        membrane glycoprotein gp130 precursor - human (;Speciles: Homo sapiens (man) (C;Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 09-Ju-C;Accession: A36337 (R;Hibi, M.; Murakami, M.; Saito, M.; Hirano, T.; Taga, T.; Kishimoto, R;Hibi, M.; Murakami, M.; Saito, M.; Hirano, T.; Taga, T.; Kishimoto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
A36337
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C;Keywords: glycoprotein; transmembrane protein

F;1-24/Domain: signal sequence #status predicted <SIG>

F;25-622/Product: prolactin receptor, long form #status

F;36-221/Domain: cytokine receptor homology <CRS>

F;59,104,233/Binding site: carbohydrate (Asn) (covalent)
                                                                                                                                            A;Cross-references: GDB:126725; OMIM:600694
A;Map position: 5q11-5q11
C;Keywords: glycoprotein; membrane protein
F;134-316/Domain: cytokine receptor homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:S78505; NID:g999114; C;Genetics:
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A; Cross-references: UNI
                                                                                                                                                                                                                                                                         A;Cross-references:
C;Genetics:
                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-918 <HIB>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
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                                                Matches
                                                                                              Query Match
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42 ISPODPTILIGSSLLATCSVHG----DPPGATAEGLYWTLNGRRLPPELSRVLNASTLALA
                                                87;
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37.1%;
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Pred. No. 5.5e-18;
                                                                          Pred. No.
                                                                                              Score 323;
                                                                                                                                                 УБотошоч
                                                                                                                                                                                                                                                                                                GB:M57230; NID:g186353; PIDN:AAA59155.1; PID:g186354
                                                   Mismatches 151;
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                                                                          4.5e-17;
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                                                                                                 Length 918;
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99

LANLNGSRQRSGDNLVCHARDGSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGA 158 ISPESPVVQLHSNFTAVCVLKEKCMDYFHVNANYIVWKTNHFTIPKEQYTIINRTASSVT

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receptor.

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C.Species: Mus musculus (house mouse)
C.Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
C.Accession: 149699; 148370
R.Saito, M.; Yoshida, K.; Hibi, M.; Taga, T.; Kishimoto, T.
J. Immunol. 148, 4066-4071, 1992
A;Title: Molecular cloning of a murine IL-6 receptor-associated
A;Reference number: 148370; MUID:92291532; PMID:1602143
A;Accession: 149699
                                                                                                                                                                                                                                                                                                                                                                                    S
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C;Keywords: glycop
F;134-314/Domain:
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A; Residues: 1-917 < RE2 >
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A; Residues: 1-917 < RES>
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                                                                                                                                                                                  KVSSESINFDPVDKVKPTPPYNLSVTNSEELSSILKLSWVSSGL--GGLLDLKSDIQYRT
                                                                                                                                                                                                                                                                                                                                                                                        LANLNGSRQRSGDNLVCHARDGSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGA 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VTŚDHINFDPVYKVKPNPPHNLSVINSEELSSILKLTWTN-PSIKSVII-LKYNIQYRTK 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ARŚDVLTLDILDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVE 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FTDIASLNIQLTCNILTFGQLEQNVYGITIISGLPPEKPKNLSCIVNEGKKMRCEWDGGR
                                                                                                                                                                                                                        SARSDVLTLDILDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRV 277
                                                                                                                                                                                                                                                          --ETYLETNYTLKSE--WATEKFPDCQSKHGT---SCMVSYMPTYYVNIEVWVEAENALG
                                                                                                                                                                                                                                                                                                     HGETFLHTNYSLKYKLRWYGQD-NTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLG 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ISPODPTILIGSSILATCSVHG----DPPGATAEGLYWTLNGRRLPPELSRVLNASTLALA 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IT-YEDRP 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STPRSERP 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DASTWSQIPPEDTASTRSSFTVQDLKPFTEYVFRIRC----MKEDGKGYWSDWSEEASG 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DSVDWKVV---DDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAA 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --ETHLETNFTLKSEWATHKFADCKAKRDT--PTSCTVDYSTVYFVNIEVWVEAENALGK 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGS 218
                     GTTYEDRPSRP
                                                             AST--PRSERP 343
                                                                                                                                                                                                                                                                                                                                                  FTDVVLPSVQLTCNILSFGQIEQNVYGVTMLSGFPPDKPTNLTCIVNEGKNMLCQWDPGR
                                                                                                                                                                                                                                                                                                                                                                                                                            IYPEFPVVQRGSNFTAICVLKEACLQHYYVNASYIVWKTNHAAVPREQVTVINRTTSSVT
                                                                                                   KDASTWIOVPLEDTMSPRTSFTVQDLKPFTEYVFRIR----SIKDSGK-GYWSDWSEEAS 316
                                                                                                                                        EDSVDWKVV---DDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTA 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.9%; Score 317.5; DB 2; ilarity 29.6%; Pred. No. 1.2e-16; Conservative 50; Mismatches 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytokine receptor homology <CRS>
                     327
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Endocrinology 135, 269-276, 1994
Endocrinology 135, 269-276, 1994
A;Title: Cloning, expression, and mutational analysis of
A;Reference number: 150455; MUID:94283267; PMID:7516866
A;Accession: I50455
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A44257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prolactin receptor - pigeon
C;Species: Columba livia (domestic pigeon)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                               C;Keywords: transmembrane proceptor homology <CRS>F;134-315/Domain: cytokine receptor homology <CRS>
                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:P40190 A;Experimental source: liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genomics 14, 666-672, 1992
A;Title: Molecular cloning a
A;Reference number: A44257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       interleukin-6 signal transducing molecule gp130 - C;Species: Rattus norvegicus (Norway rat) C;Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 C;Accession: A44257
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F;36-220/Domain: cytokine receptor homology <CRS1>
F;240-426/Domain: cytokine receptor homology <CRS2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-830 < CHE>
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                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; not A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: A44257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R; Wang, Y.; Nesbitt, J.E.; Fuentes, N.L.; Fuller, G.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-918 <WAN>
                                                                                                                                                                                                     Query Match
Best Local S
Matches 93
                                                                                                                                                                                                                                                                                                                          ;Note: sequence extracted from NCBI backbone (NCBIP:118488
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Similarity 36.6%;
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                                                                                                                                                                                                                        Similarity
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TPGAHGETFLHTNYSLKYKLRWYGQD-NTCEEYHTVGPHSCHIPKDLALFTPYEIWVEAT 213
                                        SSVTFTDVVFQNVQLTCNILSFGQIEQNVYGITILSGYPPDIFTNLSCIVNEGKNMLCQL 146
                                                                            LALALANINGSRORSGDNLVCHARDGSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRW 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YIVQIHCKP-----DHHGSWSEWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YFVQVRCNPFGIYGSKKAGIWSEWS 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KPYLVLTW-SPPPLADVRSGWLTLDYELRLKPBEAEEWETI-FVGQQTHYKMFSLNPGKK 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EDQLSVRWVSPPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTV 305
                                                                                                                       IYPEFPVVQRGSNFTATCVLKEKCLQVY----SVNATYIVWKTNHVAVPKEQVTVINRTA
                                                                                                                                                               ISPODPTILIGSSILATC-----SVHGDPPGATAEGLYWTLNGRRLPPELSRVLNAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPEKPTIIKCRSPEKETFTCWWKPGSDGG---HPTNYTLLYSKEGEERVYECPDYKTAGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                     13.7%; Score 314.5; DB 29.7%; Pred. No. 2e-16; tive 51; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and characterization of the ; MUID:93052397; PMID:1427893
                                                                                                                                                                                                                                                                                                                                                                                                                              compared
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                                                                                                                                                                                                                                                                                                                                                                                                                                conceptual translation
                                                                                                                                                                                                                                            DB 2;
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A;Cross-references: UNIPROT:P05710; GB:M74152; NID:g206389; PIDN:AAA41946.1; R;O'Neal, K.D.; Yu-Lee, L.Y.
J. Biol. Chem. 269, 26076-26082, 1994
A;Title: Differential signal transduction of the short, Nb2, and long prolact
                                                                                                       R;Ali, S.; Pellegrini, I.; Kelly, P.A.
J. Biol. Chem. 266, 20110-20117, 1991
A;Title: A prolactin-dependent immune cell
A;Reference number: A41070; MUID:92041834;
A;Accession: A41070
                                                                                                                                                                                                                                                                   RESULT
A41070
                                                                        A; Molecule type: mRNA
A; Residues: 1-412 < ALI>
                                                                                                                                                                                                                                   prolactin receptor Nb2 precursor - C;Species: Rattus normalist ''
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Boutin, J.M.; Jolicoeur, C.; Okamura, H.; Gagnon, J.; Edery, M.; Shirota, Cell 53, 69-77, 1988
A;Title: Cloning and expression of the rat prolactin receptor, a member of t A;Reference number: A29884; MUID:88165059; PMID:2832068
A;Accession: A29884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prolactin receptor precursor - rat
C;Species: Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-310 < BOU>
                                                                                                                                                                                                           Species: Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;1-19/Domain: signal sequence #status predicted;20-310/Product: prolactin receptor #status pred;31-216/Domain: cytokine receptor homology <CR8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;Cross-references: UNIPROT:P05710; GB:M19304; NID:g206364;
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                                                                                                                                                                                                Accession: A41070; I55417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NT--CEEXHTVGPHSCHIPKD-LALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E-EASGTTYEDRP 325
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                                                                                                                                                                                                                                                                                                                                                                       TSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTP 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTYECPDYKTSGPNSCFFSKQYTSIWKIYIITVNATNQMGSSSSDPLYVDVTYIVEPEPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLLKGQS----PPGKPEIHKCRSPDKETFTCWWNPGTDGG--LPTNYSLTYSKE--GEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.7%;
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Pred. No. 7e-17;
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                                                                                                                                                                                                                                                                                                                                        -----DHGYWSRWSQESSVEMP
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                                                                                                                           line (Nb2) expresses PMID:1718958
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 receptor 2 precursor -
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R; Zhang, R.; Buczko, E.; Tsai-Morris, C.H.; Hu, Z.Z.; Dufau, M.L. Biochem. Biophys. Res. Commun. 168, 415-422, 1990 A; Title: Isolation and characterization of two novel rat ovarian lactogen A; Reference number: A34631; MUID:90241201; PMID:2159291 A; Accession: A34631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lactogen receptor 1 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jul-1990 #sequence_revision 09-Oct-1992 #text_change 09-Jul-2004
C;Accession: A34631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Reference number: I55417; MUID:95014432; PMID:7929319
A;Accession: I55417
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNNA
A;Residues: 1-412 <RES>
A;Cross-references: EMBL:U07567; NID:g641963; PIDN:AAA61784.1; PID:g641964
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A_iNote: the authors translated the F_i31-216/Domain: cytokine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:P05710; GB:M34083; NID:g205122; PIDN:AAA79273.1; PID:g205123
A;Note: the authors translated the codon GAG for residue 533 as Gly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-610 < ZHA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                         126 RNLTL-EVKOLKDKKTYLWVKWSPPTITDVKTGWFTMEYEIRLKPEEAEEWE-IHFTGHO
                                                                                                                                                               238 PDVHVSRVGGLEDQLSVRWV--SPPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQ 292
                                                                                                                                                                                                                                                                                                                                                                                      121 SILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184 TQFKVFDLYPGQKYLVQTRCKP-----DHGYWSRWSQESSVEMP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 SILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQD
                                                                                                                                                                                                                                                                         181 NT--CEEYHTVGPHSCHIPKD-LALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPP
                                                                                                                                                                                                                                                                                                                                  15 SLLKGQS-----PPGKPEIHKCRSPDKETFTCWWNPGTDGG--LPTNYSLTYSKE--GEK 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 TTYECPDYKTSGPNSCFFSKQYTSIWKIYIITVNATNQMGSSSSDPLYVDVTYIVEPEPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                   TTYECPDYKTSGPNSCFFSKQYTSIWKIYIITVNATNOMGSSSSDPLYVDVTYIVEPEPP 125
                                                   TSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 313; DB 2;
Pred. No. 1.6e-16;
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A;Cross-___
F;31-216/Domain:
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A; Residues: 1-610 < SHI>
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                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-292 < RES>
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                                                                                                                                                                                                                                                                                                                                                                                       ;Cross-references: UNIPROT:Q08501; GB:M22959; NI
;31-216/Domain: cytokine receptor homology <CRS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Davis, J.A.; Linzer, D.I.H.
ol. Endocrinol. 3, 674-680,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cross-references: UNIPROT:P05710; GB:M57668; NID:g206366; PIDN:AAA41938.1;
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Date: 28-Mar_1991 #sequence_revision 28-Mar-1991 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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                                                                                                                          FTPYEIWVEATNRLGSARSDYLTLDILDYVTTDPPPDVHVSRVGGLEDQLSVRWVS--PP
                                                                                                                                                                                                           NMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNT---CEEYHTVGPHSCHIPKD-LAL
                                                                                                                                                                                                                                                                                  LSRVLNASTLALANLNGSRQRSGDNLVCHARDGSILAGSCLYVGLPPEKPVNISCWSK 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PDVHVSRVGGLEDQLSVRWV--SPPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQ 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NT:-CEEYHTVGPHSCHIPKD-LALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPP 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQD 180
                                TITDVKTGWFTMEYEIRLKSEEADEWE-IHFTGHQTQFKVFDLYPGQKYLVQTRCKP---
                                                                   ALKDF---LEQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGI 317
                                                                                                      WKIYIITVNATNEMGSSTSDPLYVDVTYIVEPEPPRNLTL-EVKQLKDKKTYLWVKWLPP
                                                                                                                                                                          DKETFTCWWNPGSDGG--LPTNYSLTYSKE--GEKNTYECPDYKTSGPNSCFFSKQYTSI
                                                                                                                                                                                                                                                RNLTL-EVKQLKDKKTYLWVKWSPPTITDVKTGWFTMEYEIRLKPEEAEEWE-IHFTGHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTYECPDYKTSGPNSCFFSKQYTSIWKIYIITVNATNQMGSSSSDPLYVDVTYIVEPEPP 125
 YGSKKAGIWSEWSHPTAASTP 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOFKVFDLYPGQKYLVQTRCKP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTP 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLLKGQS-----PPGKPEIHKCRSPDKETFTCWWNPGTDGG--LPTNYSLTYSKE--GEK
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                                                                                                                                                                                                                                                                                                                     Conservative
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35.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1989
                                                                                                                                                                                                                                                                                                                     38;
                                                                                                                                                                                                                                                                                                                  Score 309.5; DB 2;
Pred. No. 1.2e-16;
8; Mismatches 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               from
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Pred. No. 1.6e-16;
6; Mismatches 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---DHGYWSRWSQESSVEMP
                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                        NID:g200481; PIDN:AAA39977.1; PID:g20048;
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A; Restauces: UNIPROT; Q08501; GB:L14811; NID:g2:A; Cross references: UNIPROT; Q08501; GB:L14811; NID:g2:R; More, R.C.; Oka, T. Gene 134, 263-265, 1993
A; Title: Cloning and sequencing of the cDNA encoding the A; Reference number: JT0671; MUID:94085788; PMID:826231
                                   A;Cross-references: GB:L13593; NID:g347398; PIDN:AAC37641.1; R;Edery, M.; Pezet, A.; Nandi, S.; Kelly, P.A. submitted to the EMBL Data Library, June 1993
                                                                                                                                                                                                                                                                                                                                   C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence revision 02-Aug-1996 #text_C;Accession: I53269; JT0671; 334356
R;Clarke, D.L.; Linzer, D.I.H.
Endocrinology 133, 224-232, 1993
A;Title: Changes in prolactin receptor expression during A;Reference number: I53269; MUID:93307149; PMID:8319571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Davis, J.A.; Linzer, D.I.H.
Mol. Endocrinol. 3, 674-680, 1989
A;Title: Expression of multiple forms
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177524
                    A; Description:
                                                                                               A; Molecule type: mRNA
A; Residues: 1-608 < MOO>
                                                                                                                                       A;Reference number: JT0671; A;Accession: JT0671
                                                                                                                                                                                                                                                                                                                                                                                                                                                              prolactin receptor, long form - C; Species: Mus musculus (house m
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A;Residues: 1-303 <RES>
A;Cross-references: UNIPROT:Q08501; GB:M22958; NID:g200479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prolactin receptor precursor - mouse C; Species: Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                         A;Accession: I53269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Title: Expression of multiple forms of tl
A; Reference number: I57699; MUID: 89261824;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DKETFTCWWNPGSDGG--LPTNYSLTYSKE--GEKNTYECPDYKTSGPNSCFFSKQYTSI 90
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                  Isolation
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S34356
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                  nucleotide
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Pred. No. 1.3e-16;
                                                                                                                                                                                                                                     GB:L14811; NID:g293769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       222
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PMID:2725531
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                cDNA prolactin
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                                                                           PID: 9347842
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A; Molecule type: mRNA
A; Residues: 1-831 <TAN>
A; Residues: 1-831 <TAN>
A; Residues: 1-831 <TAN>
A; Cross-references: UNIPROT: Q04594; DDBJ:D13154; NID: g222848; PIDN:BAA02439.1; PID: g2228
A; Cross-references: UNIPROT: Q04594
A; Experimental source: kidney
C; Keywords: glycoprotein; transmembrane protein
F; 1-23/Domain: signal sequence #status predicted <SIG>
F; 24-831/Product: prolactin receptor #status predicted <MAT>
F; 36-219/Domain: cytokine receptor homology <CRS1>
F; 339-425/Domain: cytokine receptor homology <CRS2>
F; 439-462/Domain: cytokine receptor homology <CRS2>
F; 439-462/Domain: transmembrane #status predicted <TMM>
F; 59, 91, 100, 112, 132, 262, 303, 315, 335, 647, 701, 800/Binding site: carbohydrate (Asn) (covale
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A;Molecule type: mRNA
A;Residues: 1-557,'F',559-608 <EDE>
A;Cross-references: EMBL:X73372; NID:g312696; PIDN:CAA51789.1; PID:g312697
A;Cross-references: EMBL:X73372; NID:g312696 and short form which are resulted from alte C;Comment: Prolactin receptor have long form and short form which are resulted from alte C;Comment: This long form receptor is capable of transducing a signal to milk protein ge C;Comment: receptor; transmembrane protein
F;31-216/Domain: cytokine receptor homology <CRS>
F;31-255/Domain: transmembrane #status predicted <TMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prolactin receptor precursor - chicken
(;Species: Gallus gallus (chicken)
(;Species: Gallus gallus (chicken)
(;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
(;Accession: JQ1655
R;Tanaka, M.; Maeda, K.; Okubo, T.; Nakashima, K.
Biochem. Biophys. Res. Commun. 18, 490-496, 1992
Biochem. Biophys. Res. Commun. 18, 490-496, 1992
A;Title: Double antenna structure of chicken prolactin receptor deduced from A;Reference number: JQ1655; MUID:93075121; PMID:1445292
A;Accession: JQ1655
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293003; D. Brush J., Deuel B., Dowd P., Heldens S., Schoenfeld J., Schoenfeld J., J., Vagts A., LH., Yansura D., A., Wood W.I., A., Wood W.I., a large-scale mbrane proteins: a	Gretener D., ichat JF.; shares homology with containing bases.	-like factor-1) Euteleostomi; ; Homo. TISSUE SPECIFICITY,	Q28235 cervus elap P14787 oryctolagus Q9pth9 xenopus lae Q9pti6 xenopus lae Q9pti6 xenopus lae Q9pti0 xenopus lae Q9uap8 tetraodon n Q6uap8 tetraodon n Q90w97 cynops pyrr Q616f7 cublepharis Q75s21 rana catesb Q7t121 brachydanio Q9g1w3 ursus marit O93404 oreochromis Q9xs92 trichosurus

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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Riausberg R.D., Collins F.S., Wagner L.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., WcEwan R.J., Moramson R.D., Mullahy S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rahesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
"Generation and initial analysis of more than 15,000 full-length human rand mouse cniba."
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Ott J., Boman H
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PubMed=10966616; DOI=10.1038/78765;

Elson G.C.A., Lelievre E., Guillet C.,

Froger J., Suard I., de Coignac A.B.,

Gauchat J.-F., Gascan H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "CLF associates with CLC to form a functional heteromeric ligand the CNTF receptor complex."; Nat. Neurosci. 3:867-872(2000).
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Proc. Natl. Acad. Sci. U.S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Cold-induced
Subfamily 3.
SIMILARITY:
SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Secreted.
TISSUE SPECIFICITY: Highest levels of expression observed spleen, thymus, lymph node, appendix, bone marrow, stomach placenta, heart, thyroid and ovary. Strongly expressed alfetal lung.
                                                                                                                                               stimulation by IFN-gamma, TNF-alpha and IL-6.

DOMAIN: The WSXWS motif appears to be necessary for proper protein folding and thereby efficient intracellular transport and cell-surface receptor binding.

SURFACE: COLOR TO CRUFI are the cause of cold-induced sweating syndrome (CISS) [MMI.272430]. CISS is an autosomal recessive disorder characterized by profuse sweating induced by cool surroundings (temperatures of 7 to 18 degrees Celsius). Additional abnormalities include a high-arched palate, nasal voice, depressed nasal bridge, inability to fully extend the elbows and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    involved in nervous system development.
SUBUNIT: Forms covalently linked di- and tetramers.
heteromeric complex with cardiotrophin-like cytoking
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                                                                                         kyphoscoliosis.
SIMILARITY: Belongs to the type I cytokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Induction: Up-regulated in fibroblast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    heteromeric complex with cardiotrophin-like cytokine (CLC); the CRLF1/CLC complex is a ligand for the ciliary neurotrophic factor
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fibronectin type III domains.
immunoglobulin-like C2-type domain.
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                                                                                            family of receptors
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EMBL; AF073515; AAD39681.1; -
EMBL; AF178684; AAD54385.1; -
EMBL; AY358291; AAQ88658.1; -
EMBL; BC044634; AAH44634.1; -
HSSP; P40223; 1CD9.
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GO; GO:0004872; F:receptor activity; TAS.
GO; GO:0019735; P:antimicrobial humoral response (sensu Verte.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50853; FN3; 2.
PROSITE; PS50835; IG_LIKE; FALSE NEG.
Direct protein sequencing; Disease mutation; Glycoprotein;
Direct protein domain; Phosphorylation; Receptor; Repeat;
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InterPro; IPR003961; FN III.
InterPro; IPR003957; FN IIII-like.
InterPro; IPR007110; Ig-like.
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VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAG
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Fibronectin type-III
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RESUMT 2

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CRAIL-SONG (Rel. 43, Created)

DT 29-MAR-2004 (Rel. 43), Last sequence update)

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CRAIL-MOUSE

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=15378723; DOI=10.1002/rcm.1604; Jin W.H., Dai J., Zhou H., Xia Q.C., Zou H.F., Zeng R.; "Phosphoproteome analysis of mouse liver using immobilized metafinity purification and linear ion trap mass spectrometry."; Rapid Commun. Mass Spectrom. 18:2169-2176 (2004).
                                                                                                                                                                                                                                               neonatal mice.
SUBUNIT: Forms covalently linked di- and tetramers. Forms a heteromeric complex with cardiotrophin-like cytokine (CLC); the CRLF1/CLC complex is a ligand for the ciliary neurotrophic factor receptor (CNTFR) (By similarity).
SUBCELLULAR LOCATION: Secreted (By similarity).
TISSUE SPECIFICITY: Widely expressed in the embryo. Not detected in the brain of adult mice.
DOMAIN: The WSXWS motif appears to be necessary for proper proteir DOMAIN: The WSXWS motif appears to be necessary for proper proteir
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3SUB SPECIFICITY.
DOI=10.1016/S0960-9822(99)80266-8;
DOI=5., Robb L., Farley A., Willson T.A.,
Nomura H.,
Nomura H.,
Nobb L., Rojima T., Nomura H.,
Nobb L., Rojima T., Nomura H.,
                                                                                    fibronectin type III domains.
immunoglobulin-like C2-type domain.
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HSSP; P40223; ICD9.
MGD; MGI:1340030; Crlf1.
InterPro; IPR002996; Cytkn recept_InterPro; IPR003961; FN_III.
InterPro; IPR003957; FN_III-like.
InterPro; IPR007110; IG-1ike.
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SMART; SM00060; FN3; 2.
PROSITE; PS50853; FN3; 2.
PROSITE; PS50835; IG LIKE; FR
Glycoprotein; Immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
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                                                                                                                     PPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDS
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A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant P., Frange C.,

A Raha S.S., Lòquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Lòquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., McTley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzyninski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Tonco C. T. Mayra M. A.
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Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii, Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC076526; AAH76526.1; -.
InterPro; IPR002996; Cytkn recept B/G.
InterPro; IPR003961; FN III.
InterPro; IPR003957; FN III-like.
Pfam; PF00041; fn3; 1.
SMART; SM00060; FN3; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00060; FN3; 2.
PROSITE; PS50853; FN3; 2.
SEQUENCE 389 AA; 43314 MW; E30903B99639864A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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PPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIY
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W SEQUENCE FROM N.A.

A Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,

A Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,

A Mauceli E., Bouneau L., Fischer C., Dzouf-Costaz C., Bernot A.,

A Micaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,

RA Micaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,

RA Dasilva C., Salnoubat M., Levy M., Boudet N., Castellano S.,

RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,

RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,

RA Alimont C., Skalli Z., Cattolico L., Poulain J., Berardinis Vd.,

RA Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,

RA Cruaud C., Duprat S., Brottier P., Cottanceau J., PC, Gouzy J.,

RA Farra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,

RA Kellis M., Volff J.-N., Guigs R., Zody M.C., Mesirov J.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

RA Mincker P., Lander E.S., Weissenbach J., Crollius H.R.;

"Analysis of the Tetraodon nigroviridis genome reveals the

"Analysis of the Tetraodon nigroviridis genome reveals the
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Best Local S
Matches 259
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GO; GO:0004872; F:receptor activity; IEA
InterPro; IPR002996; Cytkn recept_B/G.
InterPro; IPR003961; FN III.
InterPro; IPR008957; FN III-like.
InterPro; IPR007110; Ig-like.
Pfam; PF00041; fin; 2.
SMART; SM00060; FN3; 2.
PROSITE; PS50853; FN3; 2.
PROSITE; PS50853; IG_LIKE; 1.
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Q6UAQ5;
05-JUL-2004
05-JUL-2004
05-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Receptor.
SEQUENCE
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Eukaryota, Metazoa; Chordata; Craniatra; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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CWSRNTKDLTCSWAPGGRGETHISTQYTLKYKLRWYGKEKECEDYTHVQPYSCSITRDLH
                            CWSKNIMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHSCHIPKDLA
                                                                                                                LPSSLYRVLSPTNLSVTLAGLNASRQTSGDNLVCHHKGHILAGSCLYVGMPPAKPVNLT
                                                                                                                                                     LPPELSRVINASTLALALANINGSRQRSGDNLVCHARDGSILAGSCLYVGLPPEKPVNIS
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(TrEMBLrel. 27,
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Matches 102
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InterPro; IPR003961; FN_III.
InterPro; IPR003957; FN_III-like.
InterPro; IPR003529; Hemptrecept 1302.
InterPro; IPR010457; Lep_receptor_Ig.
Pfam; PF00041; fn3; 4.
Pfam; PF0632B; Lep_receptor_Ig; 1.
SMART; SM00060; FN3; 4.
                                                                                                                                                                                                                                                                                                                                                                                                          Signal.
SIGNAL
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Geissen M., Heller S., Pennica D., Ernsberger U., Rohrer H.; "The specification of sympathetic neurotransmitter phenotype on gpl30 cytokine receptor signaling."; Development 125:4791-4801(1998).
EMBL; AJ011688; CAB42084.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1999 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 12,
01-MAR-2004 (TrEMBLrel. 26,
Glycoprotein 130 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50853; FN3; 5.
PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
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  YEIWVEATURLGSARSDVLTLDILDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDF
                                                                                                                                    FNDTSS----LASPLTCNVLADGQIEQNIYGISVTVGLPPEKPKNLSCIVYLSPKVEWYM 149
                                                                                                                                                                              LANLNGSRORSGDNLVCHA-RDGSI----LAGSCLYVGLPPEKPVNISC-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSK 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LFTPYEIWVEASNQLGRATSDVITLDILDVVTTDPPSGVTVSRVGQLEDQLSVRWEAPPA
                                                                                        NMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHSCHIPKDLALFTP
                                                                                                                                                                                                                                                                      ISPODPTILIGSSILATCSVHG----DPPGATAEGLYWTLNGRRLPPELSRVLNASTLALA
                                                                                                                                                                                                                                                                                                                                                                                                          918
                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                          A
                                              -CTWNPGRH--TFLDTRFRLKYMWPRETFPDCIPEYVN---NSCTI-SDVQFFVN
                                                                                                                                                                                                                                                                                                                                                                                                             102495
                                                                                                                                                                                                                                                                                                                                                                                                                               26
                                                                                                                                                                                                                                                                                                                                     16.0%;
                                                                                                                                                                                                                                                                                                                                                                                                        MW:
                                                                                                                                                                                                                                                                                                                44;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                  Score 365.5; DB 2
Pred. No. 5.1e-19;
4; Mismatches 136
                                                                                                                                                                                                                                                                                                                                                                                                                               Potential.
                                                                                                                                                                                                                                                                                                                                                                                                        FE7625FF3E3613EF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 918
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                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                  136;
                                                                                                                                                                                                                                                                                                                                                                                                          CRC64;
                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                              918;
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                                                                                                                                                                                                                                                                                                             57;
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                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                WSK 145
                                              198
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                                                                                                                                                                                                                                                                      98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               307
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Query Match
Best Local S
Matches 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                057519;
057519;
01-JUN-1998
01-JUN-1998
01-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=xgpl30;
Name=xgpl30;
Xenopus laevis (African clawed frog).
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chen J., Grace A., Submitted (JAN-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gp130p1.
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART;
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315
                                                                                 281
                                                                                                            203
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                                                                                                                                                                                            169
                                                                                                                                                                                                                                                   109
                                                                                                                                                                                                                                                                                                                                                                                                                                  PF00041; fn3; 3.
PF06328; Lep_receptor_Ig;
; SM00060; FN3; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF041845; AAC03531.1;
                                                                                                                                                                                                                       97
                                                                                                                                                                                                                                                                              37
                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                      98;
                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                             PS50853; FN3; 3.
PS50853; HEWATOPO REC L F2; UNKNOWN 1.
PS01353; HEWATOPO REC L F2; UNKNOWN 1.
PS01353; HEWATOPO REC L F2; UNKNOWN 1.
P--EAP
                                                                               VDWKVV---DDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAAST
                                                                                                                                                                                                                                                                                                       VHGDPPGAT-----AEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LFQAKYQIRYRVEDSVDWKVV---DDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKK 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LEVWYEAANALGKAESDHLVFDFIEIVKPPPPRNLSVNS-GILPTVLKLSWEN--QISTV
                                                    QDWEMVPEEDTASHRDSFTLQDLLPNTVYEVSIRC---
                                                                                                                         SDVLTLDILDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDS
                                                                                                                                                                  TLSH--RWAHFGANYCRGANNSC-
                                                                                                                                                                                             SLKYKLRW----
                                                                                                                                                                                                                       LTCNVMASGHVANTLYGIFFTLGLPPDKPTNLTCIVYNQDNLTCTWDPGR--PTNLPTNY
                                                                                                                                                                                                                                                 SGDNLVCHARDGSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNY
                                                                                                                                                                                                                                                                             VHGERPFTAYCVINQTCLREDASRIYWLVKGVKVPETQYEILNQTTSSVTFENLTTLNSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSSGP 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VMELKFNIRYRISSDINWMEVPPEDTASPRISFSIQGLRPYTEYVFSIRC-----MKEDG 310
                          PRSERPGPGGGACEPRGGEPSSGP 361
                                                                                                         SETLTIDPVNIVKPNPPQLSELISSLELPNALKIEWKNPIT-
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                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chien K.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hemptrecept_1302.
Lep_receptor_Ig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FN III.
FN III-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytkn_recept_B/G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                 30.2%;
                                                                                                                                                                                                                                                                                                                                                                15.5%;
                                                                                                                                                                                          ---YGQDNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26,
                                                                                                                                                                                                                                                                                                                                    41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
Last seq
Last ann
PSRGP 323
                                                                                                                                                                                                                                                                                                                                                 Score 354; DB 2;
Pred. No. 3.6e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ::
                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence update) annotation updat
                                                                                                                                                               -----TIHSP-GFQFYIDTTFQVEATNELGIQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---- KPSKGP
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                                                                                                                                                                                                                                                                                                                                    125;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             databases
                                                       -- IHKDGHGFWSDWSELKKQVT
                                                                                                                                                                                                                                                                                                                                                             Length 881;
                                                                                                                                                                                                                                                                                                                                                                                           CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               334
                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                            - - - NAFNLKYNÍRYRPVKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ••
                                                                                                                                                                                                                                                                                                                                      60;
                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                            220
                                                                                                                                                                                                                                                   168
                                                                                                                                      280
                                                                                                                                                                  202
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RESULT 1
Q96P36
ID Q36
ID Q36
DT 011
DT 011
DT 011
DT 011
DT 011
DT 01
DT 01
RR QN Na
OC Eu.
OC Mal
OC Mal
COX NC
RR SE RR
RR SE SE
RR SE SE
RR SE SE
RR SE SE
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S Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata.

NCBI TaxID=9606.

[11] Created)

121, Created)

122, Last sequence upda

123, Last annotation upc

124, Last annotation upc

125, Last annotation upc

126, Last annotation upc

127, Primater of the primat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local :
                                                                                                                                                                                                                                                     Q96P36;
01-DEC-2001
01-DEC-2001
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8TD78
Q8TD78;
01-JUN-2002
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP;
GO; GC
GO; GC
Trott J.F., Hovey R.C., Vone Submitted (SEP-2001) to the EMBL; AF416618; AAL23914.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00041; fn3; 2.
SMART; SM00060; FN3; 2.
PROSITE; PS50853; FN3; 2.
PROSITE; PS01352; HEMATOPO REC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Trott J.F., Hovey R.C., Koduri S., Vonderhaar Submitted (MAR-2002) to the EMBL/GenBank/DDBJ EMBL; AF492470; AAM18048.1; -. HSSP; P16471; 18P3.
                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0016020; C:membrane; IEA.
GO; GO:0004892; F:hematopoietin/interferon-class
GO; GO:0004872; F:receptor activity; IEA.
InterPro; IPR002996; Cytkn recept_B/G.
InterPro; IPR003961; FN_III.
InterPro; IPR008957; FN_III-like.
InterPro; IPR008957; FN_III-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Breast tumor;
                                                              TISSUE=Placenta;
                                                                                    SEQUENCE FROM N.A.
                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                  Name=PRLR;
                                                                                                                                                                                                                               Prolactin receptor
                                                                                                                                                                                                                                                                                                                                          Q96P36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l Similarity
83; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LAV-EVKQPEDRKPYLWIKWSPPTLIDLKTGWFTLLYEIRLKPEKAAEWE-IHFAGQQTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NTCEEYHTVGPHSCHIPKD-LALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ILAGSCLYVG-LPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGOD
                                                                                                                                                                                                                                                                                                                                                                                                                                             FKILSLHPGOKYLVOVRCKP-----DHGYWSAWSPATFIQIPSGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HECPDYITGGPNSCHFGKQYTSMWRTYIMMVNATNQMGSSFSDELYVDVTYIVQPDPPLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWWRPGTDGG--LPTNYSLTYHREGETLM
                                                                                                                                                                                                                                                   (TrEMBLrel. (TrEMBLrel. )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 268 AA;
                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                          Chordata;
Primates;
                                                                                                                                                                                                                                   short
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.5%;
                                                                                                                                                                                                                                 . 19, Creat
. 19, Last
. 25, Last
rt isoform
                     Vonderhaar B.K.;
the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29;
                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 333; DB 2; 1
Pred. No. 3.3e-17;
9; Mismatches 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                 Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FBB498AB649A078C
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                                                                                                                                                                                                                                 t sequence up
t annotation
n 1b.
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                                                                                                                                                                                                                                                                                                                                          288
                                                                                                                                                                                                                                                                                                                                       B
                                                                                                                                                                                                                                                                        update)
                                                                                                                                                 Hominidae;
                                                                                                                                                                                                                                                     update)
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databases
                       databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
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RESULT 9
Q9UHJ5
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DR REAR DR REA
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GO; GO:0016020; C:membrane; IBA.

GO; GO:0004896; F:hematopoietin/interferon-class (D2 GO:0004896; F:receptor activity; IEA.

R GO; GO:0004872; F:receptor activity; IEA.

R InterPro; IPR002996; Cytkn_recept_B/G.

R InterPro; IPR003961; FN III.

IR InterPro; IPR003528; HemptreceptL_F1.

Pfam; PF00041; fn3; 2.
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Best Local S
Matches 83
                                                GO; GO:0009986; C:cell surface; IDA.
GO; GO:00042978; F:ornithine decarboxylase activator activity; NAS.
GO; GO:00042978; F:pronithine decarboxylase activity; NAS.
GO; GO:00042803; F:pronithine receptor activity; NAS.
GO; GO:00042803; F:pronithine homodimerization activity; NAS.
GO; GO:0006916; P:anti-apoptosis; NAS.
GO; GO:0007166; P:cell surface receptor linked signal transdu. . .
GO; GO:00071795; P:lactation; NAS.
GO; GO:000694; P:T-cell activation; NAS.
GO; GO:00042110; P:T-cell activation; NAS.
GO; GO:0042110; P:transmembrane receptor protein tyrosine kin. .
GO; GO:004277; P:tyrosine phosphorylation of JAK2 protein; NAS.
InterPro; IPR002996; Cytkn recept_B/G.
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01-MAY-2000
01-MAY-2000
01-OCT-2003
                                                                                           HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=20054419; PubMed=10585417; DOI=10.1074/jbc.274.50.35461; Kline J.B., Roehrs H., Clevenger C.V.; Kline J.B., Roehrs H., Clevenger C.V.;
                      InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                          EMBL:
                                                                                                                                                                                                                                                                                                                                                                                                                 prolactin receptor."
J. Biol. Chem. 274:3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Intermediate prolactin receptor isoform.
Homo sapiens (Human)
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PROSITE; PS50853; FN3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                   P16471; 1BP3.
                                                                                                                                                                                                                                                                                                                                                                                          ol. Chem. 274:35461-35468(1999).
AF166329; AAD49855.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 ILAGSCLYVG-LPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQD
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                      IPR003961; FN_III.
IPR008957; FN_III-like.
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nilarity 37.1%;
Conservative 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 25, Last annotation updat
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HemptreceptL_F1
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Pred. No. 4.3e
28; Mismatches
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01-DEC-2001
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Trott J.F., Hovey R.C., Vond Submitched (SEP-2001) to the EMBL, AF416619; AALZ3915.1; PIR; A59405; A59405. HSSP, P16471; 1BP3.
                                                                                                                                 Pfam; PF00041; fn3; 2.
SMART; SM00060; FN3; 2.
PROSITE; PS50853; FN3;
                                                                                                                                                                                             GO; GO:0007171; P:transmembrane receptor protein tyrosine kin. GO:0042977; P:tyrosine phosphorylation of JAK2 protein; ISS InterPro; IPR002996; Cytkn_recept_B/G. InterPro; IPR003961; FN III. InterPro; IPR003961; FN III-like. InterPro; IPR003961; HemptreceptL_F1.
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Mammalia; Eutheria;
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PROSITE; PS01352; HEMATOPO_REC_L_F1;
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                                                                                                                                                                                                                                                                                                        O; GO:0009986; C:cell surface; ISS.
O; GO:0042978; F:ornithine decarboxyl
O; GO:004925; F:prolactin receptor a
O; GO:004925; F:protein homodimeriza
O; GO:004803; F:protein homodimeriza
O; GO:0006916; P:anti-apoptosis; ISS.
O; GO:0007166; P:cell surface receptor
O; GO:0007595; P:lactation; ISS.
O; GO:0007595; P:transmembrane receptor
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                                                                                                        PS50853; FN3; 2.
PS01352; HEMATOPO_REC_L_F1; 1.
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Metazoa; Chordata; C
haria; Primates; (
                                                                376
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(TrEMBLrel. 19, Last
(TrEMBLrel. 25, Last
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                                                                                                                                                                                                                                                                                                                            P:anti-apoptosis; ISS.
P:cell surface receptor linked
P:lactation; ISS.
P:steroid biosynthesis; ISS.
P:T-cell activation; ISS.
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F:prolactin receptor activity; ISS.
F:protein homodimerization activity; ISS
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14.5%;
37.1%;
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Catarrhini; Hominidae;
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RESULT 11

PRLE HUMAN STANDARD

ID PRLE HUMAN STANDARD

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DT 01-AUG-1990 (Rel. 15, L
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                          MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong J., Estapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Malemson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergen E.J., Li X., Glibbs R.A., Villalon D.K., Muzny D.M., Sodergen E.J., Li X., Glibbs R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 1).

MEDLINE=99182102; PubMed=10084611; DOI=10.1210/jc.84.3.1153;

MEDLINE=99182102; PubMed=10084611; DOI=10.1210/jc.84.3.1153;

Hu Z.-Z., Zhuang L., Meng J., Leondires M., Dufau M.L.;

"The human prolactin receptor gene structure and alternative utilization: the generic promoter hPIII and a novel human pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDINE-90114212; PubMed=2558309; Boutin J.-M., Edery M., Shirota M., Jolicc Gould D., Djiane J., Kelly P.A.; Gould D., Djiane J., Kelly P.A.; "Identification of a cDNA encoding a long in human hepatoma and breast cancer cells. Mol. Endocrinol. 3:1455-1461(1989).
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R. Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                    'Characterization of a novel and soform (delta-S1 PRLr) containing
                                                                                                                                                                                                                                                                                                      domain
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Primates;
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EMBL; AF091865; AAD32032.1; JOINED.

EMBL; AF091866; AAD32032.1; JOINED.

EMBL; AF091866; AAD32032.1; JOINED.

EMBL; AF091867; AAD32032.1; JOINED.

EMBL; AF091868; AAD32032.1; JOINED.

EMBL; AF091869; AAD32032.1; JOINED.

EMBL; AF091869; AAD32032.1; JOINED.

EMBL; AF091869; AAD32032.1; JOINED.

EMBL; BC059392; AAM53203.1; -.

PR EMBL; BC059392; AAM59392.1; -.

PDB; HBB3; X-ray; B=25-235.

R FIR; A40144.

PDB; HB93; K-ray; B=25-235.

R GO; GO:0009986; C:cell surface; IDA.

GO; GO:0009986; F:cornithine decarboxylase activator activity; NAS.

R GO; GO:00042803; F:protein homodimerization activity; NAS.

GO; GO:00042803; F:protein homodimerization activity; NAS.

GO; GO:0007166; P:anti-apoptosis; NAS.

GO; GO:0007566; P:embryo implantation; TAS.

DR GO; GO:0007596; P:lactation; NAS.

GO; GO:0007596; P:steroid biosynthesis; NAS.

GO; GO:0007595; P:lactation; NAS.

GO; GO:00042977; P:tyrosine phosphorylation of JAK2 protein; NAS.

Therefore, TpR002996; Cytkn recept B/G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 25-235.

MEDLINB=95075462; PubMed=7984244; DOI=10.1038/372478a0;

Somers W., Ultsch M., de Vos A.M., Kossiakoff A.A.;

"The X-ray structure of a growth hormone-prolactin receptor

Nature 372:478-481(1994).

-!- FUNCTION: This is a receptor for the anterior pituitary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length and mouse CDNA sequences.", proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                     InterPro; IPR003961;
InterPro; IPR008957;
InterPro; IPR003528;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=2; Bynonyms=Delta-S1;
IsoId=P16471-2; Sequence-VSP_001720;
DOMAIN: The WSXWS motif appears to be necessary for proper folding and thereby efficient intracellular transport and c surface receptor binding.
DOMAIN: The box 1 motif is required for JAK interaction and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      activation.
SIMILARITY: Belongs to the type I cytokine family of Subfamily 1.
SIMILARITY: Contains 2 fibronectin type III domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 prolactin.
SUBCELLULAR LOCATION: Type I membrane protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Event=Alternative splicing; Named isoforms=2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF091870;
AF091863;
                                        PF00041; fn3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       M31661; AAA60174.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             isoId=P16471-1; Sequence=Displayed;
                                                                         007171; P:transmembrane receptor protein tyrosine kin.
42977; P:tyrosine phosphorylation of JAK2 protein; NAS
1PR002996; Cytkn_recept_B/G.
1PR003961; FN III.
1PR003967; FN_III-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HEMATOPO_REC_L_F1; 1.
                                                         HemptreceptL_F1
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                                                       191
                                                                                                                                                     122 ILAGSCLYVG-LPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQD
                                                                                                             73
                                                                                                                                        15 LFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWWRPGTDGG--LPTNYSLTYHREGETLM
                                                                                                                                                                    83;
                                                                                                                                                                          Similarity
                                                                                                                         NTCEEYHTVGPHSCHIPKD-LALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD
                                                                                           VHVSRVGGLEDQLSVRWV--SPPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQTS
                                                                   CRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTP
                                                                                                             HECPDYITGGPNSCHFGKQYTSMWRTYIMMVNATNQMGSSFSDELYVDVTYIVQPDPPLE
                                                       FKILSLHPGQKYLVQVRCKP-----DHGYWSAWSPATFIQIP
                                                                                  LAV-EVKQPEDRKPYLWIKWSPPTLIDLKTGWFTLLYEIRLKPEKAAEWE
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                                                                                                                                                                   28;
                                                                                                                                                                   Score 332; DB
Pred. No. 1.1e
28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                   By similarity.
By similarity.
N-linked (GlcNAc...
N-linked (GlcNAc...
N-linked (GlcNAc...
N-linked (GlcNAc...
Missing (in isoform 2
/FTId=VSP_001720.
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(Potential)
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J. Biol.
EMBL; S78
HSSP; P16
                                                                                                                                                                                                                                                                                                                                      Q16354
Q16354;
                                                       Fuh G., Wells J.A.;
"Prolactin receptor antagonists
cancer cell lines.";
                                                                                                                                                                                                                                                      01-NOV-1996 (TIEMBLIEL 01, C
01-NOV-1996 (TIEMBLIEL 01, L
01-MAR-2004 (TIEMBLIEL 26, L
Prolactin receptor (Fragment)
                                                                                                                  SEQUENCE FROM N.A. MEDLINE=95286597; PubMed=7768908;
                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002996; Cytkn recept B/G.
InterPro; IPR003961; FN III.
InterPro; IPR008955; FN III-11ke.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-Sprague-Dawley;
Xu C.S., Li W.Q., Li Y.C.,
                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2004; (TrEMBLrel. Ac1055.
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    ol. Chem. 270:13133-13137(1995)
$78505; AAB34470.1; -.
P16471; 1BP3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RYRVEDSVDWKVV----DDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NALGNVSSEPINFDPVDKVKPSPPHNLSVTNSEELSSILKLAWVNSGL--DSILRLKSDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NRLGSARSDVLTLDILDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IYPEFPVVQRGSNFTATCVLKEKCLQVY----SVNATYIVWKTNHVAVPKEQVTVINRTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QYRTKDASTWIQVPLEDTVSPRTSFTVQDLKPFTEYVFRIR----SIKENGK-GYWSDWS
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Last annotation update)
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Pred. No. 4.
                                                                                                                                                                                               Craniata; Vertebrata; |
Catarrhini; Hominidae;
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Sciurognathi; Muridae;
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                                                                                                                  DOI=10.1074/jbc.270.22.13133;
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                                                                             inhibit
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                                                                                                                                                                                                                 Euteleostomi;
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S.F.,
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RESULT 14
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Matches 80
                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 1).
SEQUENCE FROM N.A. (ISOFORM 1).
TISSUE=Myeloma, and Placenta;
MEDLINE=91084044; PubMeda=2261637; DOI=10.1016/0092-8674(90)90411-7;
Hibi M., Murakami M., Saito M., Hirano T., Taga T., Kishimoto T.;
Hibi M., Murakami and expression of an IL-6 signal transducer,
                                                                                                                   TISSUE=Synovium;
MEDLINE=20341529; PubMed=10880057;
MEDLINE=20341529; PubMed=10880057;
                                                                             Tanaka M., Kishimura M
Murakami M., Nakao K.;
"Cloning of novel solu
autoantibodies in rheu
                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
                                                                                                                                                                                                                                                                                                                                                              Interleukin-6 receptor beta chain precursor (IL-6R-beta) 6 signal transducer) (Membrane glycoprotein 130) (gp130) receptor) (CDw130) (CD130 antigen).
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P40189; Q9UQ41;
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence up
25-OCT-2004 (Rel. 45, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0004896; F:hematopoletin/interferon-class (D200-domain. GO; GO:0004872; F:receptor activity; IEA.
InterPro; IPR002996; Cytkn_recept_B/G.
InterPro; IPR003961; FN III.
InterPro; IPR003957; FN III-like.
InterPro; IPR003528; HemptreceptL_F1.
Pfam; PF00041; fn3; 2.
SMART; SM00060; FN3; 2.
PROSITE; PS50853; FN3; 2.
PROSITE; PS50853; FN3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HUMAN
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             MEDLINE=21269388;
Moritz R.L., Hall
                                                                                                                                                                SEQUENCE
                                        PARTIAL SEQUENCE,
                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                      Name=IL6ST;
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                                                                                                                                                                                         63:1149-1157(1990)
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                                                                    Invest.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NSCHFGKQYTSMWRTYIMMVNATNQMGSSFSDELYVDVTYIVQPDPPLELAV-EVKQPED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LPPGKPEIFKCRSPNKETFTCWWRPGTDGG--LPTNYSLTYHREGETLMHECPDYITGGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    206 AA;
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                                                                                                                                                             N.A. (ISOFORM
                                                                l soluble gp130 and detection n rheumatoid arthritis."; 106:137-144(2000).
DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES PubMed=11098061; DOI=10.1074/jbc.M009979200; N.E., Connolly L.M., Simpson R.J.; the disulfide structure and N-glycosylation sit.
                                                                                                                                                                                                                                                                                                              Primates;
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23950 MW;
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Pred. No. 8.8e-17;
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                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CED939781B3C804E CRC64;
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N-glycosylation sites
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EXAMELY, M3 (230); AAA3 (31.); -...

EXEMBLY, ABO15706; BAA78112:1; -...

PER PIR; A36337, A36337.

R PDB; 1100; NMR; @=217-325.

PDB; 111R; X-ray; A}=23-325.

PDB; 111R; X-ray; A=23-325.

PDB; 111R; X-ray; A=23-325.

PR GALEW; HGNC:6021; II.6ST.

PR GALEW; HGNC:6021; II.6ST.

PR GALEW; HGNC:6021; II.6ST.

PR GO; GO:0004915; F:interleukin-6 receptor activity; TAS.

PR GO; GO:0004924; F:cncostatin-M receptor activity; TAS.

PR GO; GO:0004924; F:cncostatin-M receptor ilinked signal transdu. ..; TAS.

PR GO; GO:0004872; F:receptor activity; TAS.

PR GO; GO:0004872; F:receptor Inked signal transdu. ..; TAS.

PR GO; GO:0004872; F:receptor III.

PR InterPro; IPR003961; FN III.

PR InterPro; IPR003952; FN III.

PR InterPro; IPR003529; Hemptreceptor Ig.

PR InterPro; IPR003529; Hemptreceptor Ig.

PR FAGNITE; PS01353; HRMATOPO REC L F2; 1.

PR PROSITE; PS01353; HRMATOPO REC L F2; 1.
                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 122-325.
MEDLINE=9816938; PubMed=5501088; DOI=10.1093/emboj/17.6.1665;
Bravo J., Staunton D., Heath J.K., Jones E.Y.;
"Crystal structure of a cytokine-binding region of gp130.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the extracellular domain of the human signal transducer gp130."; J. Biol. Chem. 276:8244-8253(2001). [4]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=P40189-2; Sequence=VSP 001684, VSP 001685;
TISSUE SPECIFICITY: Found in all the tissues and cell lines examined. Expression not restricted to IL-6 responsive cells. DOMAIN: The WSXWS motif appears to be necessary for proper protein folding and thereby efficient intracellular transport and cell-surface receptor binding.

DOMAIN: The box 1 motif is required for JAK interaction and/or activation.

DISEASE: Isoform 2 is an autoantigen found in rheumatoid arthritis (RA) but it is not specific to patients with RA.

SIMILARITY: Belongs to the type I cytokine family of receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: Signal-transducing molecule. The receptor systems for 116, LIF, OSM, CNTF, IL11 and CTI can utilize gpl30 for initis signal transmission. Binds to IL6/IL6R (alpha chain) complex, resulting in the formation of high-affinity IL6 binding sites transduces the signal. Does not bind IL6. May have a role in embryonic development (By similarity).

SUBUNIT: Heterodimer of an alpha and a beta chain.

SUBCELLULAR LOCATION: Type I membrane protein (isoform 1).

Secreted (isoform 2).

ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Subfamily 2.

SIMILARITY: Contains 5 fibronectin type III domains SIMILARITY: Contains 1 immunoglobulin-like C2-type similarity: Contains 1 immunoglobulin-like C2-type similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DATABASE: NAME=PROW; NOTE=CD guide CD130 entry; WWW="httb://www.ncbi.nlm.nih.gov/prow/cd/cd130.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                          M57230; AAA59155.1; -. AB015706; BAA78112.1; -.
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/FTId=VSP 001684.
/FTid=VSP 001684.
/FTId=VSP 001684.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cytoplasmic (Potential).
Ig-like C2-type.
Fibronectin type-III 1.
Fibronectin type-III 2.
Fibronectin type-III 3.
Fibronectin type-III 4.
Fibronectin type-III 5.
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Box 1 motif.
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Matches 87
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01-FEB-1995
05-JUL-2004
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                                                                                                                                                                                                   STRAIN-ICR; TISSUE-Macrophage; MEDLINE-92291532; PubMed=1602143; Saito M., Yoshida K., Hibi M., Taga T "Molecular cloning of a murine II-6 r transducer, gp130, and its regulated J. Immunol. 148:4066-4071(1992).
                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 H97I
                                                                                                                                                                                                                                                                                    SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                   Name=Il6st;
                                                                                                                                                                                                                                                                                                                                                                                              Interleukin-6
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                                                                                                                                                                                                                                                                                                                                                                               nterleukin-6 receptor
signal transducer) (N
SUBUNIT: Heterodimer of an alpha and a beta chain.
SUBUNIT: Heterodimer of an alpha and a beta chain.
SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: Found in tissues such as brain, heart, tispleen, kidney, lung and liver. Found in all the cell lines except BAF-B03. Expression not restricted to II6-responsive obsultopheromath. STAGE: In embryonic stem cells it is found from 6 of gestation. It reaches a peak on day 8 and gradually deciduring the rest of embryogenesis.

DOMAIN: The WSXWS motif appears to be necessary for recommendation.
                                                                                                                                FUNCTION: Signal-transducing molecule. The receptor systems for IL16, LIF, OSM, CNTF, IL11 and CT1 can utilize gp130 for initial signal transmission. Binds to IL6/IL6R (alpha chain) complex, resulting in the formation of high-affinity IL6 binding sites, transduces the signal. Does not bind IL6. May have a role in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOUSE
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Pred. No. 8.7e-16;
2; Mismatches 151
                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D813F3672DD10D53 CRC64
                                                                                                                                                                                                                 T., Kishimoto T.;
receptor-associated
d expression in vivo.
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                                                                                                                                                                                                                                                                                                                                                                               (IL-6R-beta)
130) (GP130).
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; Murinae; Mus.
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 proper protein
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IYPEFPVVQRGSNFTAICVLKEACLQHYYVNASYIVWKTNHAAVPREQVTVINRTTSSVT ISPODETILIGSSILATCSVHG----DPPGATAEGLYWTLNGRRLPPELSRVLNASTLALA 98

90

Similarity 29. 92; Conservative

50;

Pred. No. 2.3); Mismatches

.3e-15;

Indels

23;

Gaps

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Query Ma
Best Loc
Matches
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InterPro; IPR002996; Cytkn_recept_B/G.
InterPro; IPR003961; FN III.
InterPro; IPR003961; FN_III-like.
InterPro; IPR00357; FN_III-like.
InterPro; IPR003529; Hemptrecept_1302.
InterPro; IPR003529; Hemptrecept_1302.
InterPro; IPR003529; Hemptrecept_1302.
InterPro; IPR00457; Lep_receptor_IG.
Pfam; PF00041; fn3; 4.
Pfam; PF00041; fn3; 4.
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PIR; 149699; 149699.
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PROSITE; PS01353; HEMATOPO REC L F2;
Glycoprotein; Immunoglobulin domain;
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modified and this statement is not removed.
entities requires a license agreement (See l
or send an email to license@isb-sib.ch).
                                                                  SEQUENCE
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M83336; AAA37723.1;
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Search completed: February 24, 2005, 03:36:05 Job time: 175 secs

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11601.796 Million cell updates/sec
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AR429062 Sequence
AR534953 Sequence
AY358291 Homo sapi
AF164089 Sequence
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BC044637 U4 belong
BD204627 U4 belong
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BD138607 Novel cyt
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46.1	46.1	46.1	46.1	46.1	46.8	46.8	46.8	48.4	48.5	48.5	48.6	48.6	48.6	48.6	54.3	54.3	54.3	56.2	56.2	58.7	60.3			62.9	
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REFERENCE AUTHORS TITLE JOURNAL LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE RESULT 1 A97100 FEATURES ORGANISM source 1 (bases 1 to 1716) KOSCO-Vilbois, M. and Gauchat, J. NOVEL CYTOKINE RECEPTORS Patent: WO 9920755-A 24 29-APR-1999; KOSCO VILBOIS MARIE (CH); GAUCHAT JEAN Location/Qualifiers unidentified unclassified. Sequence 24 from Patent A97100 unidentified A97100.1 GI:6780518 A97100 /organism="unidentified" /mol_type="unassigned DNA" /db_xref="taxon:32644" 1716 bp WO9920755. DNA FRANCOIS linear PAT 26-JAN-2000

ALIGNMENTS

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276

216 607

667 GCTCCTCCCTGCTGGCCACCTGCTCAGTGCACGGAGACCCACCAGGAGCCACCGCCGAGG

726

GAGCCGGATCAGGAGCCCACACAGCTGTGATCAGTCCCCAGGATCCCACGCTTCTCATCG GAGCCGGATCAGGAGCCCACACAGCTGTGATCAGTCCCCAGGATCCCCACGCTTCTCATCG

GCTCCTCCCTGCTGGCCACCTGCTCAGTGCACGGAGACCCACCAGGAGCCACCGCCGAGG

215 606

666 275

CGCGGCCGCCGCCGTTGCTGCCC---CTGCTGCTGCTCTGCGTCCTCGGGGCGCCGC

550

Best Loc Matches

490 1586;

96

Local Similarity

Conservative

75.6%; Score 1572.4; DB 6; 99.7%; Pred. No. 1.8e-288; tive 0; Mismatches 1;

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Length 1716;

Indels

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Query Match

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RS Elson,G., Gauchat,J.F. and Vilbois,M.K.

Novel cytokine receptors

AL Patent: JP 2002508922-A 14 26-MAR-2002;

GLAXO GROUP LTD

OS Unidentified
PN JP 2002508922-A/14
PD 26-MAR-2002
PF 14-OCT-1998 JP 2000517076
PF 16-OCT-1998 JP 2000517076
PF 16-OCT-1998 JP 2000517076
PF 16-OCT-1998 JP 2000517076
PF 16-OCT-1998 JP 2000517076
PC C12N15/09,A61X31/7088,A61X38/00,A61X39/395,A61X39/395,A61X45/ PC
C12N15/09,A61X31/7088,A61X38/00,A61X39/395,A61X45/ PC
PC A61P3/04,A61P35/00,A61P37/02,C07K14/715,C07K16/28,C12P21/02/,PC
PC C12N15/00,A61X37/02
CC Novel cytokine receptors
FH Key 1..1716
FT source /oranism='Unidentified'.
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Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
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Elson,G.C.A., Graber,P., Los
Menoud,L.N., Wells T.N.C., K
Direct Submission
Submitted (14-APR-1998) Dept
Research Institute, 14, Chem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1716)
Elson, G.C., Graber, P., Losberger, C., Herren, S., Gretener, D., Menoud, L.N., Wells, T.N., Kosco-Vilbois, M.H. and Gauchat, J.F. Cytokine-like factor-1, a novel soluble protein, shares homology with members of the cytokine type I receptor family J. Immunol. 161 (3), 1371-1379 (1998)
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Homo Bapiens cytokine-like factor-1
complete cds.
AF059293
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/note="similar to cytokine type-1
similar to the sequence presented
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119. .1387
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l precursor (CLF-1) mRNA,
                                                                                                      precursor"
                                                                                                                                                           receptor family members; in GenBank Accession
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                           TGAGCGTGCGCTGGGTGTCGCCACCCCGCCCTCAAGGATTTTCCTCTTTTCAAGCCAAATACC
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/note="putative"
230. .1384
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119. . 229
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/note="putative"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Location/Qualifiers
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                 TGACCACGGACCCCCCGCCCGACGTGCACGTGAGCCGCGTCGGGGGGCCTGGAGGACCAGC
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131. 1399
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GETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLG
SARSDVLTLDILDVYTTDPPDYHVSRVGGLEDOLSVRWSPPALKDFLFQAKYQIRY
RVEDSVDMKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPT
AASTPRSERPGPGGGACEPRGGEPSSGPVRRELKQFLGWLKKHAYCSNLSFRLYDQWR
AWMQKSHKTRNQDEGILPSGRRGTARGPAR"
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Pred. No. 1.8e-288;
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Elson, G. and Gauchat, J.F.
Scscntfr/nnt-1 fusion protein
Patent: WO 0155219-A 5 02-AUG-2001;
                                                          Eukaryota;
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Location/Qualifiers
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PQDPTLLIGSSLLATCSYHGDPPGATAEGLYWTLMGRRLPELSRVLMASTLALAM
LMGSRQRSGBNLVCHARDGSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAH
LMGSRQRSGBNLVCHARDGSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAH
GETFLHTNYSLKYKLRWYGQDNTCEBYHTVGPHSCHIFKDLALFTYEIWVEATNRLG
GARSDVLTLDILDVVTTDPEDVHYSRVGGLEDGDSVRWVSPFALKDFLFQAKYQIRY
RVEBSVDWKYVDDVSNOTSCRLAGLKYGTVYFVQVRCNFPGIYGSKKAGINSKWSHFPT
RVEBSVDWKYVDDVSNOTSCRLAGLKYGTVYFVQVRCNFFGIYGSKKAGINSKWSHFPT
RASTFRSERPGPGGGACEPRGGEPSSGPVRRELKQFLGMLKKHAYCSNLSFRLYDQWR
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/db_xref="GI:15394283"
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/db_xref="taxon:9606"
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Patent: JP 2002511268-A 5 16-APR-2002;
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PF 09-APR-199 JP 2000543614
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Db 1476 GCACCTGAGCCACCCTCAGCAGGAGCTGGGCTGAGCTCCAACGGCCATAACAG 1926	Qy 1687 CCTGGATGCAGAAGTCGCACAAGACCCGCAACCAGGACGAGGAGGATCCTGCCCTCGGGCA 1746	Qy 1507 CCACAGCCGCCTCCACTCCCCGCAGTGAGCGCCCGGGCCGGGCGGG	Db 876 TGAGCGTGGGTGGGTGGGCACCCCCCCTCAAGGATTTCCTTTTCAAGCCAAATACC 935 Qy 1327 AGATCCGCTACCGAGTGGAGGACAGTGTGGACTGGAACTGTGAGCAACT 1386 Qy 1327 AGATCCGCTACCGAGTGGAGGACAGTGTGGACTGGAACTGTGAGCAACT 1386 Db 936 AGATCCGCTACCGAGTGGAGGACAGTGTGGACTGGAACTGTGACCAACTGTGAGCAACC 995 Qy 1387 AGACCTCCTGCCGCCTGGCCGGCCTGAAACCCGGCACCGTGTACTTCGTGCAAGTGCGCT 1446 Db 996 AGACCTCCTGCCGCCTGGCCGGCCTGAAACCCGGCACCGTGTACTTCGTGCAAGTGCCCT 1055 Qy 1447 GCAACCCCTTTGGCATCTATGGCTCCAAGAAAGCCGGGATCTGGAGTGAGT	Qy 1087 ACTCCTGCCACATCCCCAAGGACCTGGCTCTTTACGCCCTATGAGATCTGGGTGGAGG 1146	Qy 967 GCCGCTGGACGCCAGGGGGCCACGGGGGAGACCTTCCTCCACACCAACTACTCCCTCAAGT 1026

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The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment Genome Res. 13 (10), 2265-2270 (2003)
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AASTPRSERPGFGGGACEPRGGEPSSGPVRRELKQPLGWLKKHAYCSNLSFRLYDQWR
AWMQKSHKTRNQDEGILPSGRRGTARGPAR"
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/clone="DNA38113"
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Q	B &	dg Qy	dd Qy	94 64	Query Match Best Local Sin Matches 1586;	ORIGIN			CDS	27.170.0	JOURNAL	JOURNAL REFERENCE AUTHORS	REFERENCE AUTHORS TITLE	SOURCE	ACCESSION VERSION VERSION	RESULT 11 AF073515 LOCUS	д 4	
727 GCCTCTACTGGACCCTCAATGGGCGCCGCCTGCCCCTGAGCTCTCCCGTGTACTCAACG 786	667 GETECTECTIGETIGACETICATICAGITICAGITICACIGACACACCACGAGAGCACCACCACGAGAGCACCACCAGAGCACACCAC	GAGCCGGATCAGGAGCCCACACACAGCTGTGATCAGTCCCCAGGATCCCACGCTTCTCATCG	550 CGCGGCGGCCGCCGTTGCTGCCCCTGCTGCTGCTGCGTCCTCGGGGCGCCGC 606	490 GCGCCCCGGCAGCGCCGCCCATGCCCGCCGGCCGCCGCCGCCCCAATCCG 549	/ Match 75.6%; Score 1572.4; DB 9; Length 1804; Local Similarity 99.7%; Pred. No. 1.8e-288; nes 1586; Conservative 0; Mismatches 1; Indels 3; Gaps 1;	AMMQKSHKTRNQDEGILPSGRRGTARGPAR"	, L dalb i di l'ula "infendence per l'elle le llelle un deserve en le	/product="cytokine type 1 receptor CRLP-1 precursor" /protein_id="AAD39681.1" /db_xref="GI:5166395"	/map=19p12" /map=19p12" 2041472 /note="soluble hematopoietic cytokine receptor" /codon start-1	/db /mo /or	Submitt Moncous		1 (bases Magrangeas Cloning and hematbpoie	Homo bapiens (human) M Homo bapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	complete cds. AF073515 AF073515.1 GI:5106394	4	1668 CTCCCCATTACCTAGGGCCCCTCCAAAAGA 1697	
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01 CCACGTGGAGACGCAGAGGCCGAAACTGGGGCCACCTCTGTACCCTCACTTCAGG	1441 GACGGGGCACGGCGAGAGGCCCAGATAAGCTGTAGGGGCTCAGGCCACCCTCCCT	81 47		1587 CGCGGGGCGGAAGCCGAAGCTCGGGCCGCGCGCCCCAAGCCCAAGCAGCAGGAGCAGGAGCAGGAGG	CCACAGCGCCTCCACTCCCCGCAGTGAGCGCCCGGGCCGGGCGGG	47 GCAACCCCTTTGGCATCTATGGCTCCAAGAAAGCCGGGATCTGGAGTGAGT	1387 AGACCTCCTGCCGCCTGGCCGGCCTGAAACCCCGGCACCGTGTACTTCGTGCAAGTGCGCT 1446	1327 AGATCCGCTACCGAGTGGAGGACAGTGTGGAACTGGAAGGTGGTGGACGATGTGAGCAACC 1386	1267 TGAGCGTGGGTGTCGCCACCGGCCCTCAAGGATTTCCTCTTTCAAGCCAAATACC 1326	1207 TGACCACGGACCCCCGCCCGACGTGCACGTGAGCCGCGTCGGGGGCCTGGAGGACCAGC 1266	1147 CCACCAACCGCCTGGGCTCTGCCCGCTCCGATGTACTCACGCTGGATATCCTGGATGTGG 1206	1087 ACTCCTGCCACAFCCCCAAGGACCTGGCTCTTTACGCCCCTATGACATCTGGGTGGAGG 1146	ACAAGCTTAGGTGGTATGGCCAGGACAACACATGTGAGGAGTACCACACAGTGGGGCCCC	J 14	907 TGCCCCAGAGAAACCCGTCAACATCAGCTGCTGGTCCAAGAACATGAAGGACTTGACCT 966 	847 ACCTCGTGTGCCACGCCGTGACGGCAGCATCCTGGCTGGC	787 CCTCCACCTIGGCTCIGGCCCIGGCCAACCTCAAIGGGTCCAGGCAGCGGTCGGGGGACA 846	421 GCCTCTACTGGACCCTCAACGGGCGCCCCCCGCCCCTGAGCTCTCCCCGTGTACTCAACG 480

Qy 910 CCCCAGAGAAACCCCGTCAACATCAGCTGCTGGTCCAAGAACATGAAGGACTTGACCTGCC	QY 850 TCGTGTGCCACGCCCGTGACGGCAGCATCCTGGCTGGCTCCTGTCTATGTTGGCCTGC	OY 790 CCACCTTGGCTCTGGCCCTGGCCAACCTCAATGGGTCCAGGCAGCGGTCGGGGGAACCAACC	Qy 730 TCTACTGGACCCTCAATGGGCGCCGCCCTGAGCTCTCCCCGTGTACTCAACGCCT	Qy 670 CCTCCCTGCTGGCCACCTGCTCAGTGCACGAGAACCCACCAGGAGCCACCGAGGAGGCC	Qy 610 CCGGATCAGGAGCCCACACAGCTGTGATCAGTCCCCAGGATCCCACGCTTCTCATCGGCT	recccc	CGCCCCGGCAGCCCGCCCATGCCCGCCGCCGCCGGGGCCCCGCCCCCCCC	Query Match 75.6%; Score 1572; DB 6; Length 1813; Best Local Similarity 99.7%; Pred. No. 2.1e-288; Matches 1587; Conservative 0; Mismatches 0; Indels 5; Gaps	Bource	Foster, D.C., Adams, R.L. and Lehner, J.M. Manmalian cytokine-like receptor 5 Patent: US 6271343-A 3 07-AUG-2001; Location/Oualifiers	NISM NCE	GI:16235033		1741 CTCCCCATTACCTAGGCCCCTCCAAAAGA	Db 1681 AGGGTTGGTTAGGGGCCCCTCGAAAAGA 2076	1621	1867 1561
969 Qy	909 dy 484 Db	849 47 424 Db	789 CV 364 Db	729 Oy Db	669 Qy Db	609 Qy 184 Db	549 Oy 124 Db	1, pb	Q Q	Qy B	Qy dd	Qy Db	-2001 Pb	Qу	1740 Pb	1680 Qy	1926 UD QY 1620 I Db
1985 TGAGGGTTGGTTGAGTTGCCTAGAACCCCTGCCAGGGCTGGGGGTGAGAAGGGGAGTCAT 2044	23 AGCTCTGACTCCCACGTGAGGCCACCTTTGGGTGCACCCCAGTGGGTGTGTGT		S : IGCCACGTIGAGACGCAGAGGCCGAACCCAGACTGGGCCACCTCTCTTCACCTCCACCTTCACACTT	45 CAGACGGGGACGGCAAGGCTCCTGCCAGATAAGCTTTAGGGGCTCAGGCCACCCTCCC	65	30 TCAAGAAGCACGCGTACTGCTCCAACCTCAGCTTCCGCCTCTACGACCAGTGGCGAGCCT		CAGCCGCCTCCACTCCCCGCAGTGAGCGCCCGGGGCCGGGCGGG	50 ACCCCTTTGGCATCTATGGCTCCAAGAAAGCCGGGATCTGGAGTGAGT	1390 CCTCCTGCCGCCTGGAAACCCGGCACCGTGTACTTCGTGCAAGTGCGCTGCA 1449	1330 TCCGCTACCGAGTGGAGGACAGTGTGGACTGGAAGGTGGTGGACGATGTGAGCAACCAGA 1389	1270 GCGTGCGCTGGGTGTCGCCACCCGCCCTCAAGGATTTCCTCTTTCAAGCCAAATACCAGA 1329	1210 CCACGGACCCCCGCCCGACGTGCACGTGAGCCGCGTCGGGGGCCTGGAGGACCAGCTGA 1269	1150 CCAACCGCCTGGGCTCTGCCCGCTTCCGATGTACTCACGCTGGATATCCTGGATGTGGTGA 1209	1090 CCTGCCACATCCCCAAGGACCTGGCTCTCTTTACGCCCTATGAGATCTGGGTGGAGGCCA 1149	1030 AGCTTAGGTGGTATGGCCAGGACAACACATGTGAGGAGTACCACACAGTGGGGGCCCCACT 1089	985 CCCCAGAGAAACCCGTCAACATCAGCTGCTGGTCCAAGAACATGAAGGACTTGACCTGGC 549 970 GCTGGACGCGAGGGGCCCACGGGGAGCCTTCCTCCACACCAACTACTCCCTCAAGTACA 1029

1469 CTCTGACTCCCACGTGAGGCCACCTTTGGGTGACCCCAGTGGGTGTGTGT	Db	Db 389 ACCTCGTGTGCCACGCCCGTGACGGCATCCTGGCTGGCTCCTGCTCTATGTTGGCC 448 Oy 907 TGCCCCCAGAGAAACCCCGTCAACATCAGCTGCTGGTCCAAGAACATGAAGGACTTGACCT 966
9	S &	QY 847 ACCTOGTGTGCCACGCCGGTGACGGAGGATCCTGGCTGGCTGCTTGTTTGGCC 906
1867 GCACCTGAGCCACCCTCAGCAGGAGCTGGGGCCCTGAGCTCCAACGGCCATAACAG 	Db Qy	787 CCTCCACCTTGGCTCTGGCCCAACCTCAATGGGTCCAGGCAGCGGTCGGGGGACA 84
349	B 8	OY 727 GCCTCTACTGGACCCTCAATGGGCGCCGCCTGCCCCCTGAGCTCTCCCGTGTACTCAACG 786
747	γ θ γ 2	QY 667 GCTCCTCCTGCTGGCCACCTGCTCAGTGCACGGAGACCCACCACGAGGAGCCACCGCGAGG 726
229	P 5	Qy 607 GAGCCGGATCAGGAGCCCACACACTGTGATCAGTCCCCAGGATCCCACGCTTCTCATCG 666
627 169	, B &	QY 550 CGCGGCGGCCGCCGTTGCTGCCGCCTGCTGCTGCTGCTGCGGGCGCCGC 606
109	B &	Qy 490 GCGCCCCCGGCAGCGCCCATGCCCATGCCCGCCGGCCGGGCCCCAATCCG 549
049	, B &	Query Match 75.6%; Score 1570.8; DB 6; Length 1690; Best Local Similarity 99.7%; Pred. No. 3.6e-288; Matches 1585; Conservative 0; Mismatches 2; Indels 3; Gaps 1;
47	o da	source RIGIN
1387 AGACCTCCTGCCCTGGCCGGCCTGAAACCCGGCACCGTGTACTTCGTGCAAGTGCGCT	Db Qy	Foster,D.C., Adams,R.L. and Lehner,J.M. Mammalian cytokine-like receptor 5 Patent: US 6271343-A 1 07-AUG-2001; Location/Oualifiers
1327 AGATCCGCTACCGAGTGGAGGACAGTGTGGAACGTGGAGGATGTGAGCAACC	Qy Db	NISM NCE ORS
1267 TGAGCGTGGGTGGGTGTCGCCACCCGCCCTCAAGGATTTCCTCTTTCAAGCCAAATACC	pb qq	AR164088 AR164088.1 GI:16235032 Unknown
1207 TGACCACGGACCCCCGCCCGACGTGCACGTGAGCCGCGTCGGGGGCCTGGAGGACCAGC	p	RESULT 14 AR164088 AR164088 LOCUS AR164088 1690 bp DNA linear PAT 17-OCT-2001 DEFINITION Sequence 1 from patent US 6271343.
1147 CCACCAACCGCCTGGGCTCTGCCCGCTCCGATGTACTCACGCTGGATATCCTGGATGTGG	Db Db	1589 CTCCCCATTACCTAGGGCCCCTCCAAAAGA
1087 ACTCCTGCCACATCCCCAAGGACCTGGCTCTTTACGCCCTATGAGATCTGGGTGGAGG 	Qy dd	
1027 ACAAGCTTAGGTGGTATGGCCAGGACAACACATGTGAGGAGTACCACACAGTGGGGGCCCC	Qy db	1987 AGGGTTGGGTTGCCTAGAACCCCTGCCGGGGTGGAGAAAGGGAGTCATTA
967 GCGGCTGGACGCCAGGGGGCCCACGGGGAGACCTTCCTCCACACCACCACTACTCCCTCAAGT	.Qy	1409 GCACCTGAGCCACCCTCAGCAAGAGCTGGGGTGGCCCCTGAGCTCCAACGGCCATAACAG
449 TGCCCCCAGAGAAACCCCGTCAACATCAGCTGCTGGTCCAAGAACATGAAGGACTTGACCT	da	OV 1867 GCACCTGAGCCACCCTCAGCAGGAGCTGGGGTGGCCCTGAGCTCCAACGGGCCATAACAG 1926

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        source
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Wadan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J. W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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                              Clone distribution: MGC clone distribution through the I.M.A.G.E. Consortium/ILML at: Series: IRAL Plate: 44 Row: o Column: 22. Location/Qualifiers
                                                                                                                                                       Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Akhter,N.A., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
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Maduro,C.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIAMIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (17-JAN-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1744)
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                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www.nisc.nih.gov/
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaithersburg, Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg,R.
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factor 1, mRNA
                                                                                  information can be found http://image.llnl.gov
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Best Local Similarity
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ACAAGCTTAGGTGGTATGGCCAGGACAACACATGTGAGGAGTACCACACAGTGGGGCCCC
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AWMQKSHKTRNQDEGILPSGRRGTARGPAR"
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Pred. No. 3.6e-288;
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AGGGTIGGTIGAGTIGCCTAGAACCCCTGCCAGGGCTGAGAGGGGAGTGATA 2	927 CTCTGACTCCCACGTGAGGCCACCTTTGGGTGCACCCCAGTGGGTGTGTGT	00 4	a 4.	1747 GACGGGCACGGCGAGAGGTCCTGCCAGATAAGCTGTAGGGGCTCAGGCCACCCTCCCT	1687 CCTGGATGCAGAAGTCGCACAAGACCCGGCAACCAGGACGAGGGGATCCTGCCCTCGGGCA 1746	627 245	567 185	1507 CCACAGCCGCCTCCACTCCCCGCAGTGAGCGCCCGGGCCCGGGCGGG	1447 GCAACCCCTTTGGCATCTATGGCTCCAAGAAAGCCGGGATCTGGAGTGAGT	1387 AGACCTCCTGCCGCCTGGCCGGCCTGAAACCCGGCACCGTGTACTTCGTGCAAGTGCGCT 1446 	1327 AGATCCGCTACCGAGTGGAGGACAGTGTGGACTGGAAGGTGGTGGACGATGTGAGCAACC 1386	1267 TGAGCGTGCGCTGGGTGTCGCCACCCGCCCTCAAGGATTTCCTCTTTCAAGCCAAATACC 1326	1207 TGACCACGGACCCCCCCCGACGTGCACGTGAGCCGGCGTCGGGGGGCCTGGAGGACCAGC 1266	1147 CCACCAACCGCCTGGGCTCTGCCCGCTCCGATGTACTCACGCTGGATATCCTGGATGTGG 1206	1087 ACTCCTGCCACATCCCCAAGGACCTGGCTCTCTTTACGCCCTATGAGATCTGGGTGGAGG 1146
087 ACTICCTOCCACATCCCCAAGAACCTGGCTCTTTACGCCCTNTGAGATCTAGGCAGGGGGGGGGG	087 ACTICCTGCCAACHCCCCAAGACCTGGCTCTCTTTACGCCCTATGACATTCTGGATGGA	087 ACTCCTGCCAACTCCCCAAGAACTGGCTTCTTTTAGGCCTATGAGTCTGGGGGGGG	097 ACTCCTGCCACATCCCCAAGAACCTGGCTCTTTACGCCCTATGACATCTGGGTGGAAGG	087 ACTICCTSCCAAATCCCCAAGGACCTTGCTTCTTTACGCCCTTACGACTTTGGGTTGGAGGAGTTCCCTAAGGACCTTGGGTTGGAGTTTTACGCCCTTATCAGATCTTGGGTTGGAGGTTTCCTTGGTTGG	087 ACTICCTGCCACATCCCCAAGGACCTGGCTCTTTTACGCCCTATGAGATCTGGGTGGAGG 114	087 ACTCCTGCCACATCCCCAAGGACCTGGCTCTTTACGCCCTATGAGATCTGGGTGGAGG 114	087 ACTCCTGCCACATCCCCAAGGACCTGGCTCTTTACGCCCTATGAGATCTGGGTGGAGG 114	087 ACTCCTGCCACATCCCCAAGGACCTGGCTCTTTACGCCCTATGAGATCTGGGTGGAGG	087 ACTCCTGCCACATCCCCAAGGACCTGGCTCTTTACGCCCTATGAGATCTGGGTGGAGG 114	087 ACTCCTGCCACATCCCCAAGGACCTGGCTCTTTACGCCCTATGAGATCTGGGTGGAGG 114	087 ACTCCTGCCACATCCCCAAGGACCTGGCTCTTTACGCCCTATGAGATCTGGGTGGAGG 114	087 ACTCCTGCCACATCCCCAAGGACCTGGCTCTTTACGCCCTATGAGATCTGGGTGGAGG 114	087 ACTCCTGCCACATCCCCAAGGACCTGGCTCTCTTACGCCCTATGAGATCTGGGTGGAGG 114	087 ACTCCTGCCACATCCCCAAGGACCTGGCTCTCTTACGCCCTATGAGATCTGGGTGGAGG 114	

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tive itati	Fabri M;	OPERATIONS	J-00003327 J-00007489	2000WO-AU001216		Location/Qualif 5131778 /*tag= a /product= "Muri		yt a	receptor,	ed) entry)		DNA;		1269	1391	1498 1391	1882	1579	1579	1650	2154	1804	1804	1790 1802	1790 1790	1790	1790	1790
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complex comprising NR6 and cann proliferation, differentian	LJ, Reid K, Bartlett PF,	LTD.		•		ualifiers "Murine haemopoietin receptor,		<pre>complex; haemopoietin receptor CLC; therapy; prophylaxis; pr al; neurotrophic activity; ds.</pre>	, NR6 DNA.			BP.	ALIGNMENTS	ADL13625	AAD04196	AAZ34614 AAV27144	ADF71799	AAX90753	AAV10894 AAV41689	ABQ88148	ADQ23242	ADV04231 ADV018850	ABQ88147 ADI:13624	ADN00410 AAA46902	ADG63443 ADH43172	ADE71500	ABX75462	אספפרעע
NR6 and cardiotrophin-like- differentiation and/or survival	Hilton DJ;					or, NR6 protein"		eptor; NR6; s; proliferation; ; ds.						Adl13625 Osteoarth	Aad04196 cDNA clon	Aaz34614 Human rec Aav27144 Nucleotid	Adf71799 cDNA for	Aax90753 Human U4	Aav41689 Nucleotid	Abq88148 Human ost	Adq23242 Human sof	Adn04231 Antipsori Adq18850 Human sof	Abq88147 Human ost	Adn00410 Human cDN Aaa46902 cDNA enco	Adg63443 Human cDN Adh43172 Human cDN	Human	Abx75462 Human sec	S Human

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             This is the nucleotide sequence of a cDNA clone encoding a novel type 1 cytokine receptor (see AAY05782) that has been termed human GBRI-IIR as it is believed to be an interleukin receptor, or at least a substantial part of such a receptor. To clone the cDNA, a 310 bp PCR product was amplified from human lung cDNA using primers designed from human ESTs that had been identified using the WSXWS motif of the mouse IL-13 receptor alpha 1 as query, and used as a probe to screen a human placental cDNA library. The GBRI-IIR receptor has also been identified i mice (see AAY05783), and the high degree of conservation of amino acids between the human and murine polypeptides indicates that this receptor i functionally important. GBRI-IIR nucleic acids are used for the recombinant production of GBRI-IIR polypeptides, nucleic acids, agonists, and primers. GBRI-IIR polypeptides, nucleic acids, agonists,
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                                                                                                                                                                                                                                                                                                         or mouse type I cytokine receptors hGBRI-ILR or mGBRI-ILR, creating e.g. cancer, immune disorders, obesity and AIDS.
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Use of genes and their expression profiles associated with osteoblast differentiation for screening modulators bone formation, for diagnosing or treating e.g. osteoporosis, or as markers for the differentiation
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Mertz
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SEQ ID NO

78pp + Sequence Listing;

The invention relates to genes and their expression profiles are used CC for: (a) screening modulators of precursor stem cell differentiation into CC osteoblasts, or bone tissue deposition; (b) diagnosing abnormal CC deposition of bone tissue, abnormal rate of osteoblast formation or CC cited in (b), or monitoring the progression of bone tissue deposition. CC cited in (b), or monitoring the progression of bone tissue deposition. CC osteoporosis or male osteoporosis, osteoporosis, glucocorticoid CC osteoporosis or male osteoporosis, osteoporosis, glucocorticoid CC induced abnormalities in bone formation or bone loss, conditions that CC induced abnormalities in bone formation or bone loss, conditions that CC induced abnormalities in bone formation or bone loss, conditions that CC skeletal disease linked to breast cancer, mastocytosis, Fanconi syndrome CC or fibrous dysplasia. The present sequence is that of an osteoblast CC differentiation associated CDNA marker of the invention. Note: The CC sequence data for this patent did not form part of the printed CC specification, but was obtained in electronic format directly from WIPO Car firm with a continuous contracts. ftp.wipo.int/pub/published_pct_sequences

Sequence 1716 BP; 295 A; 623 C; 525 G; 273 T; 0 U; 0 Other;

75.6%; 99.7%;

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Human; gene; ss; gene expression; bone formation; cartilage formation; embryonic development; cytokine receptor-like factor 1; CLRP-1; CLRP-1; mesenchymal cell differentiation; matrix metalloproteinase 23; MMP23; bone development; antegonist; agonist; catherin; CD68; cytokine; diagnosis; osteodystrophy; osteohpertrophy; osteoblastoma; osteopertrusis; osteogenesis imperfecta; osteoporosis; osteopenia; osteopenia; osteoma; osteoblastoma; periodontal disease; hyperparathyroidism; hypercalcaemia of malignancy; Paget's disease; osteolytic lesion; bone metastasis; bone loss; immobiliastion; sex hormone deficiency; inflammatory disease; rheumatoid arthritis; osteoarthritis;
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Determining the difference between levels of expression of a number genes, useful for diagnosing and treating disorders associated with or cartilage formation or resorption such as osteoporosis and bone of

Page 190-192; 197pp; English

The invention discloses a method for determining the difference between CC the levels of expression of a number of, at least 500 genes, during bone CC or cartilage formation. The method comprises determining levels of RNA CC from the genes to obtain levels of expression and comparing these to a CC essential process in embryonic development and plays a critical role in CC many diseases and conditions in humans. Two genes found to be regulated CC 1 (CLF-1 or CLRP-1), which is specifically regulated during bone and cartilage formation are the cytokine receptor-like factor C (CLF-1 or CLRP-1), which is specifically regulated during mesenchymal CC computer program for analysing levels of expression of a number of genes (C compositions comprising a number of antagonists or agonists of genes, CC compositions comprising whether a subject has, or is likely to CC develop, a disease related to bone or cartilage formation or resorption, for identifying a compound for treating, modulating or stimulating at treatment intended to bone or cartilage formation possibly acting as a cadherin or CD68 agonist or a cytokine antagonist. The methods and compositions are useful for costeoblastoma, osteopertrusis, osteogenesis imperfecta, osteoporosis, osteopenia, osteopertrusis, osteopenia, periodontal disease,

RESULT 4 ABX14013

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ds; breast Breast cancer prognosis marker ADR25220 standard; 05-AUG-2004. 21-OCT-2004 15-JAN-2003; 2003US-00342887 15-JAN-2004; WO2004065545-A2 ROSETTA INPHARMATICS LLC. NETHERLANDS CANCER INST. cancer; 2004WO-US001100 (first DNA; prognosis; entry) 1716 ВP gene #1081 expression;

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The present sequence encodes a human CLF-1 protein. The specification CC describes a complex comprising a NNT-1 protein and a CLF-1 and/or CC scNTFRAlpha protein. The NNT-1/CLF-1 complex is used to modulate activity CC of the scNTFRAlpha/gpl30/LIFRbeta receptor complex, or to induce CC phosphorylation of the tyrosine of gpl30 and LIFRbeta, particularly where CC cells expressing the receptor complex are in the central or peripheral CC nervous system, in neurons implicated in neuro-muscular function or in CC skeletal muscle. The complex or antibodies are also used to decrease the CC survival, growth or proliferation of tumour cells or to facilitate the CC proliferation and/or inhibit differentiation of cells stocks. The complex CC is also used to modulate activity of the gpl30/LIFRbeta receptor or cells CC expressing that receptor, particularly those cells implicated in the CC immune, haematopoietic, nervous or reproductive system, the liver or CC immune, haematopoietic, nervous or reproductive system, the liver or CC exception and Huntington's disease, to repair or regenerate nervous or parkinson's and Huntington's disease, to repair or regenerate nervous or parkinson's show the disease, to repair or regenerate nervous or improve fertility, particularly to avoid endometriosis and/or assist blastocyst implantation, thrombosis, or retinal disease, particular
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A complex comprising a NNT-1 protein and a CLF-1 and/or sCNTFRalpha protein useful to treat neurodegenerative disease including Parkinson's and Huntington's, obesity and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-JAN-2000; 2000FR-00001035.
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                                   Novel polypeptides and polynucleotides used for treatment of diseases and disorders e\cdot g\cdot immune disorders or deficiencies fungal, parasitic or viral infections.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes nucleic acids encoding PRO secreted and transmembrane proteins used therapeutically. The PRO proteins have cytostatic, anti-inflammatory, anti-proliferative and immunosuppressive activity. The proteins and polynucleotides can be used in therapy, identification of homologues, raising antibodies and design of probes and primers. They can be used in a range of diseases related to proteins that they have homology with, e.g. a PRO protein having homology to complement proteins may be used in inflammatory responses
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New isolated nucleic

acid encoding a secreted

and transmembrane (PRO)

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Eaton DL, F A, Godowski Napier MA,

Ferrara N, Filvaroff E; i PJ, Grimaldi JC, Gurno , Roy MA, Tumas D, Wood

Gurney Wood W

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97US-0069425P

97US-0069696P

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98US-007044086P

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98US-0075945P

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98US-0112850P

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Query Match
Best Local Similarity
Matches 1586; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polypeptide, for recombinantly producing the PRO polypeptide and in gene therapy.
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29-APR-1998;
22-MAY-1998;
10-JUN-1998;
10-NOV-1998;
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16-DEC-1998;
22-DEC-1998;
                                                                                                            New human nucleic acids encoding secreted and transmembrane polypeptides which are designated as PRO polypeptides are described The membrane-bound proteins have various industrial applications, including as pharmaceutical and diagnostic agents. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. Anti-PRO antibodies are useful for the affinity purification of PRO from recombinant cell culture or natural sources
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Gerritsen ME, Goddard
Hillan KJ, Kljavin IJ,
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Cornelia de:Lange syndrome; gene therapy; immune disorder;
inflammatory disease; organ failure; atherosclerosis; cardiac injury;
infertility; birth defect; premature aging; cardiac injury; AIDS; cancer;
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98US-0075945P.
98WO-US019330.
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(GETH) GENENTECH INC.

Baker KP, Gerritsen I Hillan KJ, A ME, GUL J, Kljavin J Botstein D, Eaton DL, I ME, Goddard A, Godowski Kljavin IJ, Napier MA, Eaton DL, Ferrara N, Filvaroff E; A, Godowski PJ, Grimaldi JC, Gurn Napier MA, Roy MA, Tumas D, Woo Gurney AL; Wood WI;

WPI; 2003-311003/30. P-PSDB; ABU64921.

New transmembrane polypeptides and polynucleotides useful for chromosome identification, tissue typing, gene therapy, in chromosome and gene mapping, or as molecular weight markers.

Claim 2; Fig 13; 172pp; English.

CC transmembrane polypeptide (designated as PRO proteins). 15 PRO
CC polypeptides and their encoding polymucleotides are disclosed. Also
CC polypeptides and their encoding polymucleotides are disclosed. Also
CC included are a vector comprising the PRO nucleic acid, a host cell
CC comprising the vector, a process for producing a PRO polypeptide (by
CC culturing the host cell under conditions for the expression of the PRO
CC polypeptide, and recovering the PRO polypeptide from the cell culture, an
CC isolated polypeptide having at least 80% amino acid sequence identity to
CC the PRO polypeptides, a chimaeric molecule comprising PRO fused to a
CC the PRO polypeptides, a chimaeric molecule comprising PRO fused to a
CC the PRO polypeptides, a chimaeric molecule comprising PRO fused to a
CC the PRO polypeptides, a chimaerating sense and antibody which specifically binds
CC to PRO. The PRO nucleotide sequences are useful as hybridisation probes,
CC in chromosome and gene mapping, in generating sense and antisense RNA or
CC NA, in generating transgenic or knock-out animals which can be used in
CC the evelopment and screening of therapeutically useful reagents, and in
CC gene therapy. The polypeptides may be used as molecular weight markers
CC for protein electrophoresis purposes. The PRO polypeptides and nucleic
CC colds may also be used for chromosome identification, and tissue typing.
CC RRO241 (identified as Chordin) is a candidate gene for Cornelia de Lange
CC syndrome. Other PRO proteins are variously implicated in immune
CC disorders, inflammatory disease, organ failure, atherosclerosis, cardiac
CC injury, infertility, birth defects, premature aging, cardiac injury,
CC RRO rorderin protein

Sequence 1790 BP; 359 A; 624 C; 529 ç, 278 T; 0 U; 0 Other;

S 밁 S Query Match Best Local cal Similarity 1586; Conserv 550 96 CGCGGCGGCCGCCGTTGCTGCCC---CTGCTGCTGCTCTGCGTCCTCGGGGCGCCGC 75.6%; ilarity 99.7%; Conservative Score 1572.4; Pred. No. 0; 0; Mismatches 0, ВB 1; 8 Indels Length 1790; ω --Gaps 909 155 549

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ABX78444 standard; DNA; 1790 ΒP

(first entry)

Novel human secreted protein

Human; antiinflammatory; antiarteriosclerotic; cardiant; gynecological; anti-HIV; cytostatic; antidiabetic; BMP-agonist; BMP-Antagonist; cytokine-agonist; cytokine-antagonist; gene-Therapy; inflammatory disease; organ failure; atherosclerosis; cardiac injury; inferrility; birth defect; premature aging; AIDS; cancer; diabetic complication; gene; ds.

97US-0067411P 97US-0069278P 97US-0069335P 97US-0069335P 97US-0069694P 97US-0069694P 97US-0069870P 97US-0069873P 97US-0069871P 97US-0069871P 98US-007044086P 98US-0074092P 98US-0074092P 98US-0075945P 98US-0075945P

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<sup>141</sup>lan KJ,
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11-DEC-1999
11-FEB-2000
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28-FEB-2000
                                                                                                                                                                                                                                                                                                                         The invention describes a novel isolated PRO polypeptide. The methods compositions of the present invention are useful for the diagnosis and treatment of disorders such as inflammatory disease, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, cancer, diabetic complications and mutations in general. This sequence encodes a novel human secreted PRO protein
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J, Kljavin IJ,
                                    GCCTCTACTGGACCCTCAACGGGCGCCGCCTGCCCCCTGAGCTCTCCCGTGTACTCAACG
                                                  GCCTCTACTGGACCCCTCAATGGGCGCCGCCTGCCCCCTGAGCTCTCCCCGTGTACTCCAACG
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99US-010501252

99US-01462227

99US-US01252

99US-US01252

99US-US01250

99WO-US02813

99WO-US02803

99WO-US02803

99WO-US02841

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2000WO-US005671

2000WO-US0065271

2000WO-US006520

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A, Godowski PJ, Grimaldi JC, Gu
, Napier MA, Roy MA, Tumas D, V
                                                                                                                                                                                                                                                                                                                                                                                                      English.
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   GCACCTGAGCCACCCTCAGCAGGAGCTGGGGTGGCCCCTGAGCTCCAACGGCCATAACAG
             GCACCTGAGCCACCCTCAGCAGGAGCTGGGGTGGCCCCTGAGCTCCAACGGCCATAACAG
                                                         CCACGTGGAGACGCAGAGGCCGAAACCCGAAACTGGGGCCACCTCTGTACCCTCACTTCAGG
                                                                                                     GCTCAAGAAGCACGCGTACTGCTCCAACCTCAGCTTCCGCCTCTACGACCAGTGGCGAG
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                                                                                         CCTGGATGCAGAAGTCGCACAAGACCCGCAACCAGGACGAGGGGATCCTGCCCTCGGGCA
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01-DEC-1999;

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11-FEB-2000;

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22-MAR-2000;

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                                                                       as PRO, cardiac
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                      Claim
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P-PSDB; ABU57242.
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Hillan KJ, Kljavin
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2000WO-US003565
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A, Godowski PJ, Grimaldi JC, Gu
Napier MA, Roy MA, Tumas D, W
                    English
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This invention relates to a nucleotide sequence encoding an isolated secreted and/or transmembrane protein. The nucleotide sequences of the invention may have antiinflammatory, antiarterioscilerotic, cardiant, anti-infertility, anti-HIV, cytostatic and antidiabetic activities and may be used in gene therapy. The nucleic acids and polypeptides are useful for treating inflammatory diseases, organ failure, atheroscilerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, cancer, or diabetic complications. The nucleic acids are useful as hybridisation probes, in chromosome and gene mapping, and in generating antisense RNA or DNA. The polypeptides are useful as pharmaceuticals, diagnostics, biosensors or bioteactors. Both are useful in tissue typing. The present sequence represents a nucleic acid sequence of the invention

Sequence 1790 BP; 359 A; 624 C; 529 G; 278 T; 0 U; 0 Other;

B

8;

Length 1790;

1087 1027 490 696 636 576 967 516 907 456 396 787 336 276 216 607 156 847 727 96 GAGCCGGATCAGGAGCCCACACACTGTGATCAGTCCCCAGGATCCCACGCTTCTCATCG GAGCCGGATCAGGAGCCCACACAGCTGTGATCAGTCCCCAGGATCCCCACGCTTCTCATCG CGCGGCGGCCGCCGTTGCTGCCC---CTGCTGCTGCTCTGCGTCCTCGGGGGGCGCGC CCTCCACCTTGGCTCTGGCCCTGGCCAACCTCAATGGGTCCAGGCAGCGGTCGGGGGACA GCCTCTACTGGACCCTCAATGGGCGCCGCCCTGCCCCCTGAGCTCTCCCCGTGTACTCAACG GCTCCTCCCTGCTGGCCACCTGCTCAGTGCACGAGACCCACCAGGAGCCACCGCCGAGG GCTCCTCCCTGCTGGCCACCTGCTCAGTGCACGAGACCCACCAGGAGCCACCGCCGAGG GCGCCCCGGCAGCGCCCCATGCCCGGCCGGCCGGGGCCCCGCCGCCCAATCCG CCACCAACCGCTGGGCTCTGCCCCGCTCCGATGTACTCACGCTGGATATCCTGGATGTGG ACTCCTGCCACATCCCCAAGGACCTGGCTCTCTTTACGCCCTATGAGATCTGGGTGGAGG ACTCCTGCCACATCCCCAAGGACCTGGCTCTCTTTACGCCCTATGAGATCTGGGTGGAGG ACAAGCTTAGGTGGTATGGCCAGGACAACACATGTGAGGAGTACCACACAGTGGGGCCCC GCCGCTGGACGCCAGGGGCCCACGGGGAGACCTTCCTCCACACCACCAACTACTCCCTCAAGT GCCGCTGGACGCCAGGGGCCCACGGGGAGACCTTCCTCCACACCAACTACTCCCTCAAGT TGCCCCCAGAGAAACCCCGTCAACATCAGCTGCTGGTCCAAGAACATGAAGGACTTGACCT TGCCCCCAGAGAAACCCCGTCAACATCAGCTGCTGGTCCAAGAACATGAAGGACTTGACCT CCTCCACCTTGGCCTGGCCCAACCTCAATGGGTCCAGGCAGCGGTCGGGGGACA GCCTCTACTGGACCCTCAACGGGCGCCGCCTGCCCCCTGAGCTCTCCCGTGTACTCAACG Conservative 75.6%; 0, Score 1572.4; Pred. No. 0; 0; Mismatches 1; Indels u ۲۰ Gaps 1146 155 1206 755 1086 635 575 455 846 395 786 335 726 275 999 215 695 966 515 906

TGAGCGTGCGCTGGGTGTCGCCACCCGCCCTCAAGGATTTCCTCTTTCAAGCCAAATACC

TGACCACGGACCCCCGCCGACGTGCACGTGAGCCGCGTCGGGGGGCCTGGAGGACCAGC

rctgcccgctccgatgtactcacgctggatatcctggatgtgg

TGACCACGGACCCCGCCCGACGTGCACGTGAGCCGCGTCGGGGGGCCTGGAGGACCAGC

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ABX75909
ID ABX75
XX ABX75
XX ABX75
XX ABX75
XX ABX75
XX ABX75
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DI Human
XX Human
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KW Organ
KW Organ
KW Cance
XX Cance
XX ABX75
                                                        Human; ss; gene; PRO; antiinflammatory; antiarteriosclerotic; cardiant; gynecological; anti-HIV; cytostatic; antidiabetic; inflammatory disease; organ failure; atherosclerosis; cardiac injury; infertility; birth defect; premature aging; AIDS; acquired immunodeficiency syndrome;
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Gerritsen | Hillan KJ, Baker Botstein D, n ME, Goddard *I* , Kljavin IJ, P Eaton DL, Ferrara N, Filvaroff E; A, Godowski PJ, Grimaldi JC, Gurney Napier MA, Roy MA, Tumas D, Wood F **H**

WPI; 2003-147446/14. P-PSDB; ABU56306.

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Homo sapiens

New isolated PRO polypeptide and encoding nucleic acids, useful for the diagnosis and treatment of disorders such as inflammatory disease, atherosclerosis, cardiac injury, infertility, AIDS, cancer and diabetic complications.

Claim 2; Fig 13; 171pp; English.

CC The invention relates to an isolated PRO polypeptide having at least 80% CC amino acid sequence identity to and scoring at least 80% positives when CC compared to any of 15 fully defined sequences of 235-954 amino acids, CC given in the specification. Also included are: (1) an isolated PRO CC nucleic acid having at least 80% nucleic acid sequence identity to a CC nucleotide sequence that encodes PRO or its extracellular domain, and CC comprising any of 15 fully defined nucleotide sequences of 957-3441 bp, CC 209526, 209508, 209524, 209528, 209524 and 209528, 209527, 209529, 209527, 209570, 209518, 209521 and 209619; (2) a vector CC comprising the PRO nucleic acid; (3) a host cell comprising the vector; CC (4) producing PRO polypeptides, comprising culturing the cell for expression of the PRO polypeptides, comprising culturing the PRO polypeptide and recovering the PRO polypeptide from the cell culture; (5) a chimaeric molecule comprising PRO fused to a heterologous amino acid sequence; and (6) an anti-PRP antibody. The

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Matches 1586;
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1: /cgn2_6/ptodata/1/pubpna/PCT NEW PUB.seq:

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ALIGNMENTS

US-09-037-657-43 SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 43 Sequence 43, Application UP Patent No. US20020045741A1 TITLE OF INVENTION: A NOVEL HAEMPOIETIN RECEPTOR AND GENETIC SEQUENCES TITLE OF INVENTION: ENCODING SAME FILE REFERENCE: DAVIES COLLISON CAVE (CIP) CURRENT APPLICATION NUMBER: US/09/037,657A CURRENT FILING DATE: 1998-03-10 EARLIER FILING DATE: 1998-03-10 EARLIER FILING DATE: 1997-09-11 NUMBER: 08/928,720 EARLIER FILING DATE: 1997-09-11 NUMBER OF SEQ ID NOS: 54 APPLICANT: Farley, Alison APPLICANT: Wilson, Tracy APPLICANT: Zhang, Jian-Guo APPLICANT: Alexander, Warren LENGTH: 2079
TYPE: DNA
ORGANISM: Unknown
FEATURE: APPLICANT: Kojima, Tetsuo APPLICANT: Maeda, Masatsugu APPLICANT: Kikuchi, Yasufumi APPLICANT: Nash, Andrew APPLICANT: Hilton, Douglas J. APPLICANT: Nicola, Nicos A. APPLICANT: Rakar, Steven APPLICANT: Fabri, Louis NAME/KEY: CDS LOCATION: (513)..(1775) FEATURE: INFORMATION: Application US/09037657A

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	841 GGGACAACCTCGTGTGCCACGCCCGTGACGGCAGCATCCTGGCTGG	781 TCAACGCCTCCACCTTGGCCCTGGCCCAACCTCAATGGGTCCAGGCAGCGGTCGG 840	721 CCGAGGGCCTCTACTGGACCCTCAATGGGCGCCGCCTGCCCCCTGAGCTCTCCCCTGTAC 780	661 TCATCGGCTCCTGCTGCTGCCACCTGCTCAGTGCACGGAGACCCACCAGGAGCCACCG 720	601 CGCCGCGAGCCGGATCAGGAGCCCACACAGCTGTGATCAGTCCCCAGGATCCCACGCTTC 660	541 CCCAATCCGCGCGGCGGCCGCCGTTGCTGCCCCTGCTGCTTGCT	481 CATATTTCAGCGCCCCGGCAGCGCCGGCCGCCGTGCCCGCCGGCCG	421 AGGTTCATGCTCAGGGGGCCAACTCTGTGGGTTAGGATTTGAGTTTAAGCAGCTTCTGCT 480	361 GGTTACACAGATAACTCTCTGACTTTGCCTTACAGAACCTGTGCTATTGACCTTAGGGCA 420	301 CTCAGAGGAAAGTTGTCAGATGAGCAGGTGAGTATTCTATAGCAAACAGCAAGCTAATA 360	241 TGCCTAAGCCATAGCGCGATGAGAAGGATGTATCCTATGGTGGTGATTTTCCTGTGCCCC 300	181 AGTGACAGCAAATTCTGATGTGACTGAGGGTTGGCTTGTGAAGGAGTCATTAGGAAATTC 240	121 GACTGCAGTGTCAGGGATCCAAAGGAAATGACTCCATCCCTTCCCTTTCATCCCAACCTC 180	61 TTTTTGAAAGCTAGCTGACTCACTGTTCAAGAAAGGAGAACACTTTCAATTATGCTGTTT 120	1 GCGGTATTTGTGTTTCAAATCTATCTACAGAAAAGATTGAGAACCAGAAAGCCCTTTTCGT 60	Query Match 100.0%; Score 2079; DB 9; Length 2079; Best Local Similarity 100.0%; Pred. No. 0; Matches 2079; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	; OTHER INFORMATION: Description of Unknown Organism: Nucleotide Sequence of NR6 US-09-037-657-43
Oy Db	Q B 5	S B &	?	\$ \$ \$) B &	o da Q	B &	S B 8	}) p \$?. B &	B &	8 &	B &	D &	B &	? B
1981 TGTGTGAGGGTTGGTTGAGTTGCCTAGAAACCCCCGCCAGGGCTGGGGGTGAGAAGGGGAG 2040 2041 TCATTACTCCCCATTACCTAGGGCCCCCTCCAAAAGATCC 2079		11	1 TUCUTECLACE ESPAGACIOCAMENSE CUMACICAMENTE SES CONCERTE ESTACCITACE 1 TUCCTECCACETES AGAING CASAGE CON ACTOR AC	1 CGGCAGACGGGCACACGGCACACGCCACAGATAAGCTGTAGGGGCTCAGGCCACCC CGGCAGACGGGGCACGGGGAGAGGTCCTGCCAGATAAGCTGTAGGGGCTCAGGCCACCCC CGGCCAGACAGGGGCACGGGGAGAGGTCCTGCCAGATAAGCTGTAGGGGCTCAGGCCACCCC	GGCGAGCCTGGATGCAGAAGTCGCACAAAGACCCGCAACCAGGACGAGGGGATCCTGGCCCT	TGGGCTGGCTCAAGAAGCACGGGTACTGCTCCAACCTCAGCTTCGGCCTCTACGACCACT	CCGAACCGCGGGGCGGAGAGCCGAGCTCGGGGCCGGGCGCGAGCTCAAGCAGTTCC	OI GCCACCCCACAGCCGCCTCCACTCCCCGCAGTGAGCGCCGAGGAGCGCGAGGAGCGCGAGCGA	1 TGCGCTGCAACCCCTTTGGCATCTATGGCTCCAAGAAGCCGGGATCTGGAGTGAGT	BI GCAACCAGACCTCCTGCCGCCTGGCCGGCCTGAAACCCGGCACCGTGTACTTCGTGCAAG 14 B1 GCAACCAGACCTCCTGCCGCCTGGCCGGCCTGAAACCCGGCACCGTGTACTTCGTGCAAG 14	21 AATACCAGATCCGCTACCGAGTGGAGGACAGTGTGGACTGGAAGGTGGTGGACGATGTGA 21 AATACCAGATCCGCTACCGAGTGGAGGACAGTGTGGACTGGAAGGTGGTGGACGATGTGA 21 AATACCAGATCCGCTACCGAGTGGAGGACAGTGTGAACTGGAAGGTGGTGGACGATGTGA 21 AATACCAGATCCGCTACCGAGTGGAGGACAGTGTAAAAGGTGGAAAGGTGGACGATGTGA	61 ACCAGCTGAGCGTGCGCTGGGTGTCGCCACCCGCCCTCAAGATTTCCTCTTTCAAGCCA 61 ACCAGCTGAGCGTGCGTGGGTTCGCCACCCGCCCTCAAGATTTCCTCTTTCAAGCCA	ATTINGTTARCCACGGACCCCCCCCACGTGACGTGAGCCCTCGGGGGCCTGGAGG ATTINGTGATGACCACGGACCCCCCCCCCCCCACGTGACGTGAGCCCCGCCTCGGGGGCCTTGGAGG ATTINGTGATGACCACGGACCCCCCCCCCCCCCCCACGTGACCGTGAGCCCCGCCTCGGGGGCCTTGGAGG ATTINGTTGATCACCGACCTGGACCTGAACGTGAGCCCTCGGGGGCCTTGGAGG ATTINGTTGATCACCGACCTGGACGTGAACGTGAGCCCTCGGGGGCCTTGGAGG ATTINGTTGATCACCGACCTGGACGTGAACGTGAGCCTCGGGGGCCTTGGAGG ATTINGTTGATCACCGACCTGAACGTGAACGTGAGCCGCGTCGGGGGCCTTGGAGG ATTINGTTGATCACCACGTGAACGTGAACCTGAGACGTGAGCCTTCGAGGGCCTTGGAGG ATTINGTTGATCACCACGTGAACGTGAACCTGAGACGTGAGACCTTCGAGGGCCTTGGAGG ATTINGTTGATCACCACGTGAACGTGAACCTGAGACGTGAGCCTTCGAGGGCCTTGGAGG ATTINGTTGATCACCACGTGAACGTGAACCTGAGACGTGAGACCTTCGAGGGCCTTGGAGG ATTINGTTGATCACCACGTGAACGTGAACGTGAACCTGCGCGTCGGGGGCCTTGGAGG ATTINGTTGATCACCACCTTGAACCTTGAACCTGCGCGTTCGGGGGCCTTGGAGG ATTINGTTGATCACCACCTTGAACGTGAACGTGAACCTTCGAGGGCCTTGGAGGCCTTGAACGTGAACCTCCACACGTGAACGTGAACACACAC	41 TGANGGCCACCAACCGCCTGGGCTCTGCCCGCTCCGATGTACTCACGCTGGATATCCTGG 41 TGGAGGCCACCAACCGCTGGGCTCTGCCCCGCTCCGATGTACTCACGCTGGATATCCTGG	B1 GGCCCACTCCTGCCACATCCCCAAGGACCTGGCTCTCTTTACGCCCTATGAGATCTGGG	21 1 CANGTACANG LIAGGING IA ING CANGACAM CACA IS ING CANGANG INC CACACAGING INC INCIDENTIAL INCIDENTIA	61 TGACCTGCCGCTGGACGCCAGGGGGCCCACGGGGGAGACCTTCCTCCACACCAACTACTCCC

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LENGTH: 1716

TYPE: DNA

ORGANISM: Homo sapi
FEATURE:
NAME/KEY: CDS
LOCATION: (119)..(1
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Publication No. US20030087259A1
GENERAL INFORMATION:
APPLICANT: CLÂNCY, BRIAN M.
APPLICANT: PÍTTMAN, DEBRA M.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOI
TITLE OF INVENTION: CARTILAGE FORMATION
FILE REFERENCE: GIA-002.01
CURRENT APPLICATION NUMBER: US/10/125,691
CURRENT FILING DATE: 2002-04-18
PRIOR APPLICATION NUMBER: 60/284,786
PRIOR APPLICATION NUMBER: 60/284,786
PRIOR FILING DATE: 2001-04-18
NUMBER OF SEQ.ID NOS: 4
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO. 1
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Best Local Similarity 99.7%;
Matches 1586; Conservative
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                                    GCCGCTGGACGCCAGGGGCCCCACGGGGAGACCTTCCTCCACACCAACTACTCCCTCAAGT
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RESULT 3
US-10-172-118-1081
; Sequence 1081, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue

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APPLICANT: Mao, Mao
APPLICANT: Van 't Veer, Laura
APPLICANT: Van 't Veer, Laura
APPLICANT: Van 't Veer, Marc
APPLICANT: Van de Vijver, Marc
APPLICANT: Bernards, Rene
TITLE OF INVENTION: Diagnosis and Prognosis of
FILE REFERENCE: 9301-175-99
CURRENT APPLICATION NUMBER: US/10/172,118
CURRENT FILING DATE: 2002-05-14
PRIOR APPLICATION NUMBER: 60/380,770
PRIOR FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 2699
SEQ ID NO 1081
TENDETH: 1716
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ORGANISM: Homb sapiens
PUBLICATION INFORMATION:
DATABASE EXCEBSION NUMBER: NM 004750
DATABASE ENTRY DATE: 2001-06-18
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Linsley, Peter
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Pred. No. 0;
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RESULT 4

US-10-342-887-1081

; Sequence 1081, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
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APPLICANT: Van 't Veer, Laura Johanna
APPLICANT: Van de Vijver, Marc J.
APPLICANT: Van de Vijver, Marc J.
APPLICANT: Bernards, Rene
ITILE OF INVENTION: Diagnosis and Prognosis of
FILE REFERENCE: 9301-188-99
CURRENT APPLICATION NUMBER: US/10/342,887
CURRENT APPLICATION NUMBER: 60/298,918
PRIOR APPLICATION NUMBER: 60/298,918
PRIOR FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: 60/380,710
PRIOR APPLICATION NUMBER: 10/172,118
PRIOR APPLICATION NUMBER: 10/172,118
PRIOR FILING DATE: 2002-05-14
PRIOR FILING DATE: 2002-06-14
INUMBER OF SEQ ID NOS: 2699
SEQ ID NO 1081
LENGTH: 1716
TYPE: DNA
ORGANISM: Homo sapiens
US-10-342-887-1081
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Best Local S
Matches 1586
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Similarity 99.7%;
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                                              CCACCAACCGCCTGGGCTCTGCCCGCTCCGATGTACTCACGCTGGATATCCTGGATGTGG
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Pred. No. 0;
0; Mismatches
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US-10-329-056-1
; Sequence 1, Application US/10329056
; Publication No. US20040073377A1
; GENERAL INFORMATION:
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APPLICANT: Pittman, Debra D.
APPLICANT: Clancy, Brian M.
APPLICANT: Clancy, Brian M.
TITLE OF INVENTION: Methods and compositions
FILE REFERENCE: 01997.028800.1
CURRENT APPLICATION NUMBER: US/10/329,056
CURRENT FILING DATE: 2002-12-23
PRIOR APPLICATION NUMBER: US 10/125,691
PRIOR FILING DATE: 2002-04-18
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; PRIOR APPLICATION NUMBER: US 60/; PRIOR FILING DATE: 2001-04-18; NUMBER OF SEQ ID NOS: 4; SOFTWARE: PatentIn version 3.1; SEQ ID NO 1; LENGTH: 1716; TYPE: DNA ; ORGANISM: Homo sapiens FEATURE: NAME/KEY: CDS; LOCATION: (119)..(1387); OTHER INFORMATION: US-10-329-056-1
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Sequence 56, Application US/10450826
PUBLICATION NO. US20040101818A1
GENERAL INFORMATION:
APPLICANT: JI, Darren
APPLICANT: Axelrod, Douglas W.
APPLICANT: Axelrod, Douglas W.
APPLICANT: Jaiswal, Neelam
APPLICANT: Eistean, Richard
APPLICANT: Houghton, Adam
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APPLICANT: Houghton, Adam
FAPPLICANT: HOUGhTON, Adam
COURENT APPLICATION INFORMATION: Gene Expression Profiles Ass
FILE REFERENCE: 044921-5039-WO
COURRENT APPLICATION NUMBER: US/10/450,826
CURRENT FILING DATE: 2003-06-18
PRIOR APPLICATION NUMBER: US 60/255,882
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; PRIOR FILING DATE: 2001-04-24
; NUMBER OF SEQ ID NOS: 149
; SOFTMARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 1716
TYPE: DNA
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RESULT 7

US-09-866-028-31

Sequence 31, Application US/09866028

Patent No. US20020058309A1

GENERAL INFORMATION:

APPLICANT: Botstein, David

APPLICANT: Eaton, Dan

APPLICANT: Forrara, Napoleone

APPLICANT: Filvaroff, Ellen

APPLICANT: Gerritsen, Mary

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Christopher

APPLICANT: Gormaldi, Christopher

APPLICANT: Girmaldi, Christopher

APPLICANT: Mjarin, Ivar

APPLICANT: Napier, Mary

APPLICANT: Wood, William

TITLE OF INVENTION: SECRETED AND TRANSM

TRANSMEMBRANE POLYPEPTIDES AND

NUCLEIC

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; TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/866,028
; CURRENT FILING DATE: 2001-05-25
; Prior application data removed - consult PAL
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 31
; LENGTH: 1790
; TYPE: DNA
; ORGANISM: Homb Sapien
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APPLICANT: Roy, Mas,
APPLICANT: Roy, Mas,
APPLICANT: Napier,
APPLICA
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                                                                             Godowski, Paul
Grimaldi, Christopher
Gurney, Austin
Hillan, Kenneth
Kljavin, Ivar
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Roy, Margaret
Tumas, Daniel
Wood, William
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Goddard, Audrey
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PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILLING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILLING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILLING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,335
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OR FILING DATE: December 12, 1997
OR APPLICATION NUMBER: 60/069,696
OR FILING DATE: December 16, 1997
IOR APPLICATION NUMBER: 60/069,694
IOR FILING DATE: December 16, 1997
IOR APPLICATION NUMBER: 60/069,702
IOR FILING DATE: December 16, 1997
IOR APPLICATION NUMBER: 60/069,870
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IOR APPLICATION NUMBER: 60/069,870
IOR APPLICATION NUMBER: 60/069,870
OR APPLICATION NUMBER: PCT/US99/28409
OR FILING DATE: NO. US20020102647ALember 30
OR APPLICATION NUMBER: PCT/US99/28313
OR FILING DATE: NO. US20020102647ALember 30
OR APPLICATION NUMBER: PCT/US99/28301
OR FILING DATE: December 1, 199
OR APPLICATION NUMBER: PCT/US99/30095
OR FILING DATE: December 16, 199
OR APPLICATION NUMBER: PCT/US90/03565
OR FILING DATE: Pebruary 11, 2000
OR APPLICATION NUMBER: PCT/US00/04414
OR FILING DATE: February 22, 2000
OR APPLICATION NUMBER: PCT/US00/05841
OR APPLICATION NUMBER: PCT/US00/05841
OR APPLICATION NUMBER: PCT/US00/05841
OR APPLICATION NUMBER: PCT/US00/05841
OR APPLICATION NUMBER: PCT/US00/08439
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OR APPLICATION NUMBER: 60/074,086

OR FILING DATE: February 9, 1998

OR APPLICATION NUMBER: 60/074,092

OR FILING DATE: February 9, 1998

OR APPLICATION NUMBER: 60/075,945

OR FILING DATE: February 25, 1998

OR FILING DATE: February 25, 1998
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PILING DATE: March 3, 1999

APPLICATION NUMBER: PCT/US99/12252

FILING DATE: June 22, 1999

APPLICATION NUMBER: PCT/US99/21090

APPLICATION NUMBER: PCT/US99/21090
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APPLICATION NUMBER: 09/218,517
FILING DATE: December 22, 1998
APPLICATION NUMBER: 09/254,311
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APPLICATION NUMBER: 60/075,945
FILING DATE: February 25, 1998
APPLICATION NUMBER: 60/112,850
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APPLICATION NUMBER: 60/060,017
FILING DATE: December 18, 1997
APPLICATION NUMBER: 60/070,440
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APPLICATION NUMBER: PCT/US98/25108
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APPLICATION NUMBER: 60/146,222
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NIMBER: PCT/US98/19330
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PRIOR FILING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: Duly 28, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR PILING DATE: Pebruary 28, 2001
NUMBER OF SEQ ID NOS: 120
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NUMBER OF SEQ ID NOS: 120
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RESULT 9
US-09-944-457-31
  APPLICANT: Baker, Kevin
APPLICANT: Botsein, Davin
APPLICANT: Botsein, Davin
APPLICANT: Beton, Dan
APPLICANT: Ferrara, Napol
APPLICANT: Filvaroff, Ell
APPLICANT: Gerritsen, Mar
APPLICANT: Goddard, Audre
APPLICANT: Goddwski, Paul
APPLICANT: Gurney, Austin
APPLICANT: Hillan, Kennet
APPLICANT: Kljavin, Ivar
APPLICANT: Kljavin, Ivar
APPLICANT: Kljavin, Ivar
                                                                                                                                    Sequence 31, Application US/09944457 Patent No. US20020110859A1 GENERAL INFORMATION:
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  Ferrara Napoleone
Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
Godowski, Paul
Grimaldi, Christopher
Gurney, Austin
Hillan, Kenneth
Kljavin, Ivar
Napier, Mary
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PRIOR FILING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: July 28, 2000
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
I SEQ ID NO 31
LENGTH: 1790
TYPE: DNA
ORGANISM: Homo Sapien
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Best Local Similarity 99.7%;
Matches 1586; Conservative
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                                                CTCTGACTCCCACGTGAGGCCACCTTTGGGTGCACCCCAGTGGGT
                                                      GACGGGGCACACGACAAGGTCCTGCCAGATAAGCTGTAGGGGCTCAGGCCACCCTTCCCTG
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RESULT 10
US-09-945-587-31
; Sequence 31, Application US/09945587
; Patent No. US20020127643A1
; GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Betstein, David
APPLICANT: Ferrara, Mapoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary
APPLICANT: Goddward, Audrey
APPLICANT: Goddwski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin

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CURRENT APPLICATION NUMBER: US/09/945,587
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR PPLICATION NUMBER: 60/067,411
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR PPLICATION NUMBER: 60/069,334
PRIOR PPLICATION NUMBER: 60/069,334
PRIOR APPLICATION NUMBER: 60/069,335
PRIOR APPLICATION NUMBER: 60/069325
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR FILING DATE: December 11, 1997
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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OR APPLICATION NUMBER: 60/06935
OR FILING DATE: December 11, 1997
OR APPLICATION NUMBER: 60/069,278
OR FILING DATE: December 12, 1997
OR APPLICATION NUMBER: 60/069,425
OR FILING DATE: December 16, 1997
OR APPLICATION NUMBER: 60/069,694
OR FILING DATE: December 16, 1997
OR APPLICATION NUMBER: 60/069,694
OR FILING DATE: December 16, 1997
OR APPLICATION NUMBER: 60/069,702
OR FILING DATE: December 17, 1997
OR APPLICATION NUMBER: 60/069,873
OR FILING DATE: December 17, 1997
OR APPLICATION NUMBER: 60/069,873
OR FILING DATE: December 17, 1997
OR APPLICATION NUMBER: 60/069,873
OR APPLICATION NUMBER: 60/069,873
OR FILING DATE: December 18, 1997
OR APPLICATION NUMBER: 60/069,017
OR APPLICATION NUMBER: 60/076,440
OR FILING DATE: Datuary 9, 1998
OR APPLICATION NUMBER: 60/074,098
OR APPLICATION NUMBER: 60/074,098
OR APPLICATION NUMBER: 60/074,098
OR APPLICATION NUMBER: 60/074,092
OR APPLICATION NUMBER: 60/074,092
OR APPLICATION NUMBER: 60/074,092
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DR FILING DATE: February 25, 1998
DR APPLICATION NUMBER: 60/112,850
DR FILING DATE: December 16, 1998
DR APPLICATION NUMBER: 60/113,296
DR FILING DATE: December 22, 1998
DR APPLICATION NUMBER: 60/146,222
DR FILING DATE: July 28, 1999
DR FILING DATE: July 28, 1999
                                                                                                                                                                                                    FILING DATE: MALL.

PILING DATE: MALL.

APPLICATION NUMBER: PCT/US-9/21090

TITING DATE: June 22, 1999/21090

TAN NUMBER: PCT/US-9/21090

TAN 15, 1999

TAN 15, 1999
                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 09/216,021
FILING DATE: December 16, 1998
APPLICATION NUMBER: 09/218,517
FILING DATE: December 22, 1998
APPLICATION NUMBER: 09/254,311
                                                         APPLICATION NUMBER: PCT/US99/28409
FILING DATE: No. US20020117643A1ember
APPLICATION NUMBER: PCT/US99/28313
FILING DATE: No. US20020127643A1ember
APPLICATION NUMBER: PCT/US99/28301
FILING DATE: December1, 1999
APPLICATION NUMBER: PCT/US99/30095
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                  FILING DATE:
APPLICATION 1
  FILING
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Kljavin, Ivar
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DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER: PCT/US98/25108
                    : December 16, 1999
NUMBER: PCT/US00/03565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER: PCT/US98/19330
September 16, 1998
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; ORGANISM: Homo
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PRIOR FILING DATE: February 22, 2000
PRIOR PPLICATION NUMBER: PCT/US00/05841
PRIOR PLIING DATE: March 2, 2000
PRIOR PILING DATE: March 2, 2000
PRIOR PILING DATE: March 30, 2000
PRIOR PPLICATION NUMBER: PCT/US00/08439
PRIOR PILING DATE: March 30, 2000
PRIOR PILING DATE: May 22, 2000
PRIOR PILING DATE: May 22, 2000
PRIOR PILING DATE: July 28, 2000
PRIOR PILING DATE: July 28, 2000
PRIOR PILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR PILING DATE: December 1, 2000
PRIOR PILING DATE: Pebruary 28, 2001
PRIOR FILING DATE: February 28, 2001
PRIOR FILING DATE: February 28, 2001
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LENGTH: 1790
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Best Local Similarity 99.7
Matches 1586; Conservative
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    Patent No. US20020132768A1
    GENERAL INFORMATION:
    APPLICANT: Baker, Kevin
    APPLICANT: Botstein, David
    APPLICANT: Ecton, Dan
    APPLICANT: Ferrara, Napoleone
    APPLICANT: Filvaroff, Ellen
    APPLICANT: Goddard, Audrey
    APPLICANT: Goddard, Audrey
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Ferrara, Napoleone
Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
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CURRENT APPLICATION NUMBER: US/09/945,015
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069335
PRIOR FILING DATE: December 11, 1997
PRIOR PILING DATE: DECEMBER: 60/069,425
PRIOR PILING DATE: DECEMBER: 60/069,425
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IOR FILING DATE: December 11, 1997

IOR APPLICATION NUMBER: 60/069, 325

IOR APPLICATION NUMBER: 60/069, 326

IOR APPLICATION NUMBER: 60/069, 327

IOR APPLICATION NUMBER: 60/069, 425

IOR APPLICATION NUMBER: 60/069, 702

IOR APPLICATION NUMBER: 60/069, 702

IOR APPLICATION NUMBER: 60/069, 702

IOR APPLICATION NUMBER: 60/069, 870

IOR APPLICATION NUMBER: 60/074, 086

IOR APPLICATION NUMBER: 60/113, 296

IOR APPLICATION NUMBER: 60/113, 296

IOR APPLICATION NUMBER: 60/146, 225

IOR FILLING DATE: December 16, 1998

IOR APPLICATION NUMBER: 60/146, 225

IOR FILLING DATE: December 17, 1998

IOR APPLICATION NUMBER: 60/146, 225

IOR FILLING DATE: December 16, 1998

IOR APPLICATION NUMBER: 60/146, 225

IOR FILLING DATE: December 16, 1998

IOR APPLICATION NUMBER: 60/121, 296

IOR APPLICATION NUMBER: 60/123, 311

IOR FILLING DATE: December 16, 1998

IOR APPLICATION NUMBER: 60/123, 302

IOR FILLING DATE: December 16, 1998

IOR APPLICATION NUMBER: 60/123, 302

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IOR FILLING DATE: December 16, 1998

IOR APPLICATION NUMBER: 60/123, 302

IOR FILLING DATE: December 16, 1998

IOR APPLICATION NUMBER: 60/123, 302

IOR FILLING DATE: December 17, 1999

IOR APPLICATION NUMBER: 60/123, 302

IOR FILLING DATE: December 10, 1998

IOR APPLICATION NUMBER: 60/123, 302

IOR FILLING DATE: 
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Tumas, Daniel
Wood, William
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Hillan, Kenneth
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PRIOR FILING DATE: December 16, 1373

PRIOR APPLICATION NUMBER: PCT/US00/03565

PRIOR PILING DATE: Pebruary 17, 2000

PRIOR APPLICATION NUMBER: PCT/US00/04414

PRIOR FILING DATE: Pebruary 22, 2000

PRIOR APPLICATION NUMBER: PCT/US00/05841

PRIOR FILING DATE: March 2, 2000

PRIOR APPLICATION NUMBER: PCT/US00/08439

PRIOR FILING DATE: March 30, 2000

PRIOR APPLICATION NUMBER: PCT/US00/14042

PRIOR FILING DATE: March 30, 2000

PRIOR APPLICATION NUMBER: PCT/US00/20710

PRIOR APPLICATION NUMBER: PCT/US00/32678

PRIOR FILING DATE: Duly 28, 2000

PRIOR APPLICATION NUMBER: PCT/US00/32678

PRIOR FILING DATE: December 1, 2000

PRIOR APPLICATION NUMBER: PCT/US01/06520

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RESULT 12
US-09-944-396-31
; Sequence 31, Application US/09944396
; Patent No. US20020132981A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
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CTCCCCATTACCTAGGGCCCCTCCAAAAGA 20/6 CTCCCCATTACCTAGGGCCCCTCCAAAAGA 1685	y 2047 b 1656	B 8
CTGCCAGGGCTGGGGGTGAGAAGGGGAGTC	159	, p
AGGGTTGGTTGAGTTGCCTAGAACCCCTGCCAGGGCTGGGGGTGAGAAGGGGAGTCATTA 2046	<u>.</u>	Ş
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CTCAAGAAGCACGCGTACTGCTCCAACCTCAGCTTCCGCCTCTACGACCAGTGGCGA	1236	Дb
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AGACCTCCTGCCGCCTGGCCAGCCTGAAACCCGGCACCGTGTACTTCGTGCAAGTGCGCT 1055	996	뫄
AGACCTCCTGCCGCCTGGCCGGCCTGAAACCCCGGCACCGTGTACCTTCGTGCAAGTGCGCT 1446	13	Q
CGAGTGGAGGACAGTGTGGACTGGAAGGTGGTGGACGATGTGAGCAAC) 936	뫄
AGATCCGCTACCGAGTGGAGGACAGTGTGGACCTGGAAGGTGGTGGACGATGTGAGCAACC 1386	13	S
TGAGCGTGCGCTGGGTGTCGCCACCCGCCCTCAAGGATTTCCTCTTTCAAGCCAAATACC 935	876	ర్జ
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CCAG	916	뫄
TGACCACGGACCCCCCCCCCGACGTGCACGTGAGCCGGGGGCCTGGAGGACCAGC 1266	1207	S S
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRA
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944,396
CURRENT FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-05-25
PRIOR PILING DATE: 2001-05-25
PRIOR PILING DATE: December 3, 1997
PRIOR PILING DATE: December 11, 1997
PRIOR PILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069335
PRIOR APPLICATION NUMBER: 60/06937
PRIOR PILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR FILING DATE: December 12, 1997
PRIOR PRIOR DATE: DECEMBER: 60/069,425
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OR FILING DATE: December 16, 1998
OR APPLICATION NUMBER: 09/218,517
OR RILING DATE: December 22, 1998
OR APPLICATION NUMBER: 09/254,311
OR FILING DATE: March 3, 1999
OR APPLICATION NUMBER: PCT/US99/12252
OR FILING DATE: June 22, 1999
OR APPLICATION NUMBER: PCT/US99/21090
OR FILING DATE: September 15, 1999
OR FILING DATE: September 15, 1999
OR APPLICATION NUMBER: PCT/US99/28409
OR APPLICATION NUMBER: PCT/US99/28409
OR APPLICATION NUMBER: PCT/US99/28313
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APPLICATION NUMBER: 16, 1997
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Gerritsen, Mary
Goddard, Audrey
Goddowski, Paul
Grimaldi, Christopher
Gurney, Austin
Hillan, Kenneth
Kljavin, Ivar
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 TE: June 22, 1999

N NUMBER: PCT/US99/21090

TE: September 15, 1999

N NUMBER: PCT/US99/28409

TE: No. US20020132981A1ember 31

N NUMBER: PCT/US99/28313

TE: No. US20020132981A1ember 3
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E: December 16, 1998
N NUMBER: 09/218,517
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: September 16, 1998
NUMBER: PCT/US98/25108
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NUMBER: 60/074,092
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NUMBER: 60/074,086
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NUMBER: 60/070,
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Matches 1586; Conservative
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OR FILING DATE: December1, 1999
OR APPLICATION NUMBER: PCT/US99/30095
OR FILING DATE: December 16, 1999
OR APPLICATION NUMBER: PCT/US00/03565
OR FILING DATE: February 11, 2000
OR APPLICATION NUMBER: PCT/US00/04414
OR FILING DATE: February 22, 2000
OR APPLICATION NUMBER: PCT/US00/05841
OR FILING DATE: March 2, 2000
OR APPLICATION NUMBER: PCT/US00/08439
OR FILING DATE: March 30, 2000
OR APPLICATION NUMBER: PCT/US00/14042
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FILING DATE: December 1, 2000
APPLICATION NUMBER: PCT/US01/06520
FILING DATE: February 28, 2001
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RESULT 13
US-09-944-432-31
US-09-944-432-31; Sequence 31, Application US/09944432; Patent No. US20020142419A1; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
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APPLICANT: TUMAS, PARISE
APPLICANT: THANS, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRA
TITLE OF INVENTION: SECRETED AND TRANSMEMBRA
TITLE OF INVENTION: SECRETED
PRICE OF INVENTION: SECRETED
THE REPERENCE: P2544891C1
CURRENT PILING DATE: 001-09-26
PRICE APPLICATION NUMBER: 00/067,411
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PRICE FILING DATE: December 11, 1997
PRICE APPLICATION NUMBER: 60/069,278
PRICE FILING DATE: December 11, 1997
PRICE APPLICATION NUMBER: 60/069,278
PRICE FILING DATE: December 12, 1997
PRICE APPLICATION NUMBER: 60/069,278
PRICE APPLICATION NUMBER: 60/069,278
PRICE FILING DATE: December 12, 1997
PRICE APPLICATION NUMBER: 60/069,694
PRICE FILING DATE: December 16, 1997
PRICE APPLICATION NUMBER: 60/069,694
PRICE FILING DATE: December 17, 1997
PRICE APPLICATION NUMBER: 60/069,904
PRICE FILING DATE: December 17, 1997
PRICE APPLICATION NUMBER: 60/069,902
PRICE FILING DATE: December 17, 1997
PRICE APPLICATION NUMBER: 60/069,903
PRICE APPLICATION NUMBER: 60/069,003
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Hillan, Kenneth
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Grimaldi,Christopher
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Goddard, Audrey
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Filvaroff, Ellen
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PRIOR FILING DATE: NO. US20020142419Alember PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: December1, 1999
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PRIOR PILING DATE: December 16, 1999
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PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: March 2, 2000
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PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR APPLICATION NUMBER: PCT/US00/32678
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PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: May 22, 2000
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PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/6520
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PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR PELICATION NUMBER: 60/067,411
PRIOR PELICATION NUMBER: 60/067,411
PRIOR PILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069335
PRIOR FILING DATE: December 11, 1997
PRIOR FILING DATE: December 11, 1997
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CURRENT APPLICATION NUMBER: US/09/943,762
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DR FILLING DATE: December 17, 1997
DR APPLICATION NUMBER: 60/68,017
DR FILLING DATE: December 18, 1997
DR APPLICATION NUMBER: 60/070,440
DR FILLING DATE: January 5, 1998
DR APPLICATION NUMBER: 60/074,086
DR FILLING DATE: FEBRUARY 9, 1998
DR APPLICATION NUMBER: 60/074,092
DR FILLING DATE: FEBRUARY 9, 1998
DR APPLICATION NUMBER: 60/074,092
DR FILLING DATE: FEBRUARY 9, 1998
                                                                        FILING DATE: December 1, 1998
APPLICATION NUMBER: 09/216,021
FILING DATE: December 16, 1998
APPLICATION NUMBER: 09/218,517
APPLICATION NUMBER: 09/218,517
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FILING DATE: December 11, 1997
APPLICATION NUMBER: 60/069,425
APPLICATION NUMBER: 12, 1997
FILING DATE: December 22, 1998
APPLICATION NUMBER: 09/254,311
FILING DATE: March 3, 1999
APPLICATION NUMBER: PCT/US99/11
FILING DATE: June 22, 1999
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FILING DATE: December 22, 1998
APPLICATION NUMBER: 60/146,222
FILING DATE: July 28, 1999
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APPLICATION NUMBER: 60/075,945
FILING DATE: February 25, 1998
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APPLICATION NUMBER: 60/069,702
FILING DATE: December 16, 1997
APPLICATION NUMBER: 60/069,870
FILING DATE: December 17, 1997
                                                                                                                                                                             FILING DATE: September 16, 1998
APPLICATION NUMBER: PCT/US98/25108
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Goddard, Audrey
Godowski, Paul
Grimaldi, Christopher
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Napier, Mary
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Hillan, Kenneth
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Filvaroff, Ellen
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  March 3, 1955
MINMBER: PCT/US99/12252
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September 16, 1998
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PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
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ORGANISM: Homo Sapien
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APPLICATION NUMBER: PCT/US00/14042
FILING DATE: May 22, 2000
APPLICATION NUMBER: PCT/US00/20710
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OR FILLING DATE: Pebruary 21, 2000
OR APPLICATION NUMBER: PCT/US00/05841
OR APPLICATION NUMBER: PCT/US00/05841
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